

24995

From: Hamud, Fozia  
Sent: Wednesday, January 22, 2003 3:59 PM  
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308-8891

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P. Sheppard  
Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
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Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:33:59 ; Search time 14 Seconds

(without alignments)  
1125.786 Million cell updates/sec

Title: US-09-714-792a-4

Perfect score: 2104  
Sequence: 1 MAFVCLAIICLYTFLISTTF.....LLLRKPNTYPKMPEFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

rchd: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	380	1132_HUMAN	014627 homo sapien
2	310.5	14.8	420	115R_HUMAN	001344 homo sapien
3	298	14.2	424	1131_MOUSE	009030 mus musculu
4	295.5	14.0	427	1131_HUMAN	P78552 homo sapien
5	263	12.5	831	1_PRLR_CHICK	004594 gallus gall
6	247	11.7	415	1_PRLR_MOUSE	P21183 mus musculu
7	238	11.3	831	1_PRLR_MEIGA	091094 meleagris g
8	220	10.5	369	1_PRLR_HUMAN	P31785 homo sapien
9	216.5	10.3	369	1_PRLR_HUMAN	090374 columba liv
10	212.5	10.1	369	1_PRLR_MOUSE	P34902 mus musculu
11	208	9.9	373	1_CYRG_MOUSE	P40321 canis fami
12	195	9.3	878	1_IL3B_MOUSE	P26954 mus musculu
13	189.5	9.0	379	1_CYRG_BOVIN	095118 bos taurus
14	178.5	8.5	897	1_CYRG_HUMAN	P32927 homo sapien
15	173.5	8.2	896	1_CYRG_MOUSE	P26955 mus musculu
16	165	7.8	581	1_PRLR_BOVIN	028172 bos taurus
17	165	7.8	610	1_PRLR_RAT	P05710 rattus norv
18	159	7.6	581	1_PRLR_SHEEP	046561 ovis aries
19	159	7.6	608	1_PRLR_MOUSE	008501 mus musculu
20	151	7.2	622	1_PRLR_HUMAN	P16471 homo sapien
21	151	7.2	862	1_1125_HUMAN	096655 homo sapien
22	150.5	7.2	917	1_IL6B_MOUSE	000560 mus musculu
23	150	7.1	581	1_PRLR_CEREL	028825 cervus elap
24	149	7.1	616	1_PRLR_RABIT	P14787 oryctolagus
25	142.5	6.8	400	1_GMCR_HUMAN	P15509 homo sapien
26	138	6.6	378	1_IL3R_HUMAN	P26951 homo sapien
27	134.5	6.4	1097	1_LIFR_HUMAN	P42702 homo sapien
28	131.5	6.2	630	1_PRLR_ORENI	091515 oreochromis
29	128	6.1	874	1_1125_MOUSE	P97378 mus musculu
30	126.5	6.0	918	1_IL6B_HUMAN	P40189 homo sapien
31	120.5	5.7	836	1_GCSR_HUMAN	099062 homo sapien
32	116.5	5.5	1282	1_DOME_DROME	09vw60 drosophila
33	113.5	5.4	1165	1_LEPR_HUMAN	P48357 homo sapien

34	112.5	5.3	1631	1_PTP1_DROME	P35992 drosophila
35	109.5	5.2	918	1_IL6B_RAT	P40190 rattus norv
36	107.5	5.1	638	1_GCSR_HUMAN	P10912 homo sapien
37	107.5	5.1	837	1_GCSR_MOUSE	P40223 mus musculu
38	107	5.1	107	1_GHR_BOVIN	P79108 bos taurus
39	106	5.0	634	1_GHR_SHEEP	028575 ovis aries
40	105	5.0	511	1_VGLG_VSVO	P04884 vesicular s
41	104.5	5.0	1092	1_LIFR_MOUSE	P42703 mus musculu
42	102.5	4.9	638	1_GHR_PIG	P19786 sus scrofa
43	101.5	4.8	638	1_GHR_RABIT	P19941 oryctolagus
44	99.5	4.7	1162	1_LEPR_RAT	062959 rattus norv
45	99	4.7	507	1_EPOR_MOUSE	P14753 mus musculu

## ALIGNMENTS

```

RESULT 1
ID 1132_HUMAN STANDARD: PRT; 380 AA.
AC 014627; 000667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13
DE binding protein).
GN IL13RA2 OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=96279273; PubMed=8663118;
RA Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N.,
RA Ferrara P.;
RT "Cloning and characterization of a specific Interleukin (IL)-13
RT binding protein structurally related to the IL-5 receptor alpha
RT chain."
RL J. Biol. Chem. 271:16921-16926(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finerty H.,
RA Henderson S.L., O'Hara R.M., Jr., Turner K.J., Wood C.R., Collins M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97321053; PubMed=9177784;
RA Guo J., Apio F., Wellerin M.P., Lebeau B., Jacques Y., Minvielle S.;
RT "Chromosome mapping and expression of the human interleukin-13
RT receptor."
RL Genomics 42:141-145(1997).
CC - FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13
CC (IL-13). BUT NOT TO IL-4.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL: X95302; CA66617.1; -
DR EMBL: U70981; AAB17170.1; -
DR EMBL: Y08768; CA470021.1; -
DR Genew: HGNC:5975; IL13RA2.

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Db 25 DEKISLLPVPNETIKVTG-LAQVLLQMKRPNPDQEO-RVNLEIYQVKNAPKREDYETRI 82
QY 87 KRLHYKDGDFLNGKIEAKIHTLLPMQCTNGSEVSSMAFTTWISPOGIPETKVDMDCV 146
Db 83 ES---KCVTILHKGFSAVKTITLQ---NDHSLASSMAAEILH-APGSGTISVNLCTGT 135
QY 147 -----YYNMOYLL-CSMKPGSIGVLLDITNLYLFY----WYEGDLHALQCVDIKAD 191
Db 136 TWTEEDNYSRLKSYQVLSLHCTWLVTGDAPEDIQYFLYRYGSMTE-----ECQETSKDT 189
QY 192 -GQNTICRPP--YLEASDYKDFYICVNGSSSEKPIRSSYFTFOLQNIYKPLDPVYLFTFR 248
Db 190 LGRTNACWEPFRTILSKGDMLSVLVNGSSKSHAIKRPEDQLFALHAIDQINPLWTAETI 249
QY 249 ESSCEIKLKWSPILPIPARCFDYETIEIRREDDTILVTANVEETTKTNTROLCPFY 308
Db 250 BFT-RLSTOWEKPVSAFPHCFDYETIKHTNRYGLQIEKLTNAFTSIIDLSKRYDVAV 308
QY 309 RSKVNIYCSDDGIMSEWSDKQCEGEDLSKTLTLPFGFILL-----VIFVTGIL 362
Db 309 RAAVSSMCREAGLWSEMS-QPIYGNDEKRP--LREW-----FVIYIMATICHTLLLSLI 361
QY 363 LRKPNTYPRMIP 374
Db 362 KRICHLMTKLPF 373

RESULT 3
1131_MOUSE STANDARD: PRT; 424 AA.
AC 009030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13A-1) (interleukin-13 binding protein) (NR4).
GN IL13RA1 OR IL13RA OR IL13R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP MEDLINE=96133964; PubMed=8552669;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
"Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";
Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
CC -1- SIMILARITY: CONTAINS AN IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; S80963; AAB50695.1; -
CC MGI; MGI:105052; Il13ral.

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DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003532; Hemitopon_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 26
FT DOMAIN 26 340
FT TRANSMEM 341 364
FT DOMAIN 365 424
FT DOMAIN 37 100
FT DISULFID 44 93
FT DISULFID 132 142
FT DISULFID 171 183
FT CARBOHYD 35 35
FT CARBOHYD 59 59
FT CARBOHYD 103 103
FT CARBOHYD 136 136
FT CARBOHYD 262 262
FT CARBOHYD 338 338
SQ SEQUENCE 424 AA; 48402 MW; EB8330AD0C82C9F9 CRC64;

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Query Match 14.2%; Score 298; DB 1; Length 424;  
 Best Local Similarity 25.8%; Pred. No. 3.4e-17;  
 Matches 108; Conservative 70; Mismatches 158; Indels 82; Gaps 21;

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QY 8 IGCLYFLIST--TPGCTSSDDEIKVNPQDEIYDPGIGLYILOMQPPLSLDFHKECT 66
Db 7 LGELLVLLMTATVGVQVAAA---TEVQPPVTNLVSVENLCTIWTWSPPEGAS--PKMT 61
QY 67 VEY-----ELKRYNIGSETWKTITIKNLHYKDFLNGKIEAKIHTLLPMQCT-NGSEVO 120
Db 62 LNFESHPDQDQKKIAPR-----HRKELPLDEKICGLQVOS---QGSANSESEP 108
QY 121 SSWAETTWIS-PQGIPEKVDMDCVYYNMOYLCSMKPGIGVLLDITNLYLFYEGDL 179
Db 109 SPLVKKC--ISPPEDPESAVTELICMHLNLSYMKCSWLPGNTPSPDRHYLYWYSSLE 166
QY 180 HALQCVDIKADGONIGCFPYLEAS---DYDFYICVNGSSSEKPIRSSYFTFOLQNIY 236
Db 167 KSRQC-ENIRREGOHACSFKLTKEPSEFHQVNOIMVADNKG--IRPSKIVSLSTIV 223
QY 237 KPLPPLYLFTRESSCEIKLKWSPILPGIPARCFDYETIEIR----- 277
Db 224 KRDP-RIKHLNLKNGALLVQKNPN-FRSCFLYEFVEVNNQTDGRHNHILEVEDKQCN 281
QY 278 -EDDTTL-----VTAIVENETYLKTTNTRQLCFVRSKVNIIYCSDDGIMSEWSDKQ 329
Db 282 SSSDNNMESTSCFOLPGVLADAVYTVRVKTKNLCF-----DDNKLMSDMSSEAO 331
QY 330 CMEGEDLSK-KTLTLPFWLPFGFILLIVFTGLLR-KPNTP-----KMIPEFCD 379
Db 332 STGKDNSTFTYTMLTITV-FVAVAVITLLFYLRKLKIIITPPIPDPEKIFKMGFD 388

RESULT 4
1131_HUMAN STANDARD: PRT; 427 AA.
AC P78552; Q29966; Q95646;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13A-1) (CD213a1 antigen).
GN IL13RA1 OR IL13RA OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Carcinoma;
RP MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,

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CC FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC FT CONFLICT 130 130 T -> I (IN REF. 3).
CC FT CONFLICT 358 358 G -> D (IN REF. 3).
CC SQ SEQUENCE 427 AA; 48759 MM; 59833BBF554107B CNC64;

Query Match 14.0%; Score 295.5; DB 1; Length 427;
Best Local Similarity 26.0%; Pred. No. 5,56-17;
Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 11 LYTFLITFECTSSDTEIKVNPPODEIYDPGLYGLYLQWOPRPLSLDHFEKTEYV- 69
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 10 LMAILLACGGGGGGGAAPETOPPTNLSVSENLCTVITWMPBEGAS--SNCSLWYF 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 70 ----ELKYRNIGSEFWTKIITKLNLYKKGDFPLNGKIGIAKHTLPLWOC--TNGSEQSSMA 124
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 68 SHFDKDKOKTAPETFRKRI-----EVLNKEITCLQVGS---QSTVSEKPSLIV 114
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 125 ETTYWIS-PQGIPEPTKYQMDCVYVNMQYLLCSMKPGIGVLDNTYNNLFYVEGDHALQ 183
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 115 EKC--ISRPEDPDSAVTELOCIMHNLSTYMCMSNLPGNNTSPDNTYLYLWHRSLKTHQ 172
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 184 CVDYIKADGONIGCRFPYLEASD--YKDEYICVNGSSSNKPIRSSYTFQLONIYKPLRP 241
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 173 C-ENIFREGGYGCSFDLTWKDSSFEGHSQVQIMWKDAGKIKFSFINVLPSRYKPPDP 231
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 242 --VLTFTRESSCKIKLWSPILGRIPARCDEYEIEHEDDT-----LYTAVENETY 293
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 232 HIKNLSPHND--DLVYQWENPQNT-SRCLFEVEVENNSQTEHNVFYVQEAECNEEF 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 294 TLKNTNETROLQCFVY-----RSKVNLYIC-SDDCIWSMSDQKQCEGDSLKK 339
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 288 ERNVENTS--CFNVPGVLPDLTNTVTRKRVKTNKLCYDDKLMSWMSQEM-----SIOKK 339
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 340 TLRFWLPLF-----GFTLLIVIEYTG--LIRKNYTP-KMIFEFCD 379
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 340 RNSTLYITMLLIVPVAIIVLLYLKRLKIIFPDPIDPGKIKFEMFCD 391
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 5
PRLR_CHICK STANDARD; PRT; 831 AA.
AC 004594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPRP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC SHRIN-White leghorn; TISSUE=Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
   the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
   PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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Db 198 TFINSGGEOLAVHNGSSKRAAIKPFQDLSPALDQVNPRTVVEIESN-SLYIGWE 256
QY 260 IPLGPAPACPDYEIEIEDD-----TTLVATVENEFTLTETMETROLCPV 308
Db 257 KPLSPFPHCHCNELKITYNTNGHOKELANKFISKIDVSTYSIO-----V 305
QY 309 RSKVNYICSDGJSEMSDKOCWEGEDISKRTLRFW---LPEGFILIVFYVTLGLLR 364
Db 306 RAAVSSPCRMGRCMGEMS-QPIYVQKE--RKSLVE-WHLIVLPACFVLLIF--SLICR 359
QY 365 KPNTPPKMIP 374
Db 360 VCHLWTRLEP 369

RESULT 7
PRLR_MEIGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (TPRLR).
CN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Zhou J.F., Zadowrony D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo."
RL Biol. Reprod. 55:1081-1090(1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE=Ovary;
RA Plits G.R., You S.K., Foster D.N., el Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC
DR EMBL: L76587; AAB01544.1; -
DR EMBL: U22947; AAA75038.1; -
DR EMBL: U22924; AAA75039.1; -
DR HSSP: P16471; 1BP3
DR InterPro: IPR002996; CRA1
DR InterPro: IPR003961; FN_III
DR InterPro: IPR003528; Hemtopoptn_L_F1
DR Pfam: PF00041; fn3; 4
DR SMART: SM00060; FN3; 3
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831 POTENTIAL.
FT DOMAIN 24 438 PROLACTIN RECEPTOR.
FT TRANSMEM 439 459 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

Query Match 11.38; Score 238; DB 1; Length 831;
Best Local Similarity 26.18; Pred. No. 6,7e-12;
Matches 97; Conservative 53; Mismatches 178; Indels 44; Gaps 17;

QY 18 TTFGCTSSDTEIKVN--PRODFE---TVDPG-----YLGTYLWQPPSL 59
Db 97 TTYNITVATNEIGSNSSDPDYVDTSTVOPGSPVNLLETORYANIMYLMKWSPLLA 156
QY 60 DHEFCEVEYELKRYNIGSETWKTITTKNLHYKDGFDLNGEAKHTLTPMOCTNGSEV 119
Db 157 DASSNHLHYHLRLKPEKEEMEV---PVGVOQCKNR-LNNGMHRVYVGRCLDPGE 212
QY 120 QSSW-AETTWISPOGIPETRVQDMDCVYVNWQYLLCSWKFGVLLDTNNTFYWEG 178
Db 213 WSEWSEERRILISGLSPPEKPTITKCRSPEKFTCMWKGDLGGHPNTYLLYSKEGE 272
QY 179 DHALQCVDTIKADONICGRPEYLEASDYKDFYICVNGSSNKRPIRSSYFPOLONTVP 238
Db 273 EGYVECPDY-RTAGPN-SCYDCKKHTSWYNTYNTKATNMGSSNDDPRHYVDTYIOP 330
QY 239 LPVYLFTRESSEIK---LKWS-IPLGPAPA--RCFDEIEIR-EDDTTLVATVEN 290
Db 331 DPPANVLTLEKKPINRKRYLMTWSPPLADVRSGWMLTLDVELRKPEEGEEMETVFQ 390
QY 291 ET-YTLKTTNTROLCPYRSKVNICSDD--GIWSESKQCKE-GEDSLKTLRLFWL 346
Db 391 QTOYKMSFLNKGKRYI-----VOIHCKPDHNGSMESENTEIPNDFVKDMI-VMI 443
QY 347 PFGFILLIVIV 358
Db 444 VLGVLSSLICLI 455

RESULT 8
CYRG_HUMAN STANDARD; PRT; 369 AA.
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common gamma chain precursor (gamma-C) (Interleukin-
DE 2 receptor gamma chain) (IL-2R gamma chain) (p64) (CD132 antigen).
GN IL2RG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=1631539;
RA Takeshita T., Asao H., Ohlani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor."
RL Science 257:379-382(1992).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE-Liver;  
 RX MEDLINE=93293887; Pubmed=8514792;  
 RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;  
 RT "Characterization of the human interleukin-2 receptor gamma chain  
 gene.";  
 RL J. Biol. Chem. 268:13601-13608(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.  
 RX MEDLINE=94004847; Pubmed=8401490;  
 RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,  
 RA Willard H., Henthorn P.S.;  
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated  
 in X-linked severe combined immunodeficiency, SCIDX1.";  
 RL Hum. Mol. Genet. 2:1099-1104(1993).  
 RN [4]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE=94090315; Pubmed=8266076;  
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,  
 RArai K.-I., Sugamura K.;  
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between  
 receptors for IL-2 and IL-4.";  
 RL Science 262:1874-1877(1993).  
 RN [5]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE=94090317; Pubmed=8266078;  
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,  
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,  
 RA Leonard W.J.;  
 RT "Interleukin-2 receptor gamma chain: a functional component of the  
 interleukin-4 receptor.";  
 RL Science 262:1880-1883(1993).  
 RN [6]  
 RP IDENTIFICATION AS A IL-7R SUBUNIT.  
 RX MEDLINE=94090316; Pubmed=8266077;  
 RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,  
 RA Leonard W.J.;  
 RT "Interleukin-2 receptor gamma chain: a functional component of the  
 interleukin-7 receptor.";  
 RL Science 262:1877-1880(1993).  
 RN [7]  
 RP 3D-STRUCTURE MODELING OF 57-248.  
 RX MEDLINE=95111955; Pubmed=7529123;  
 RA Bamorough P., Hedecock C.J., Richards W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 modelling.";  
 RL Structure 2:839-851(1994).  
 RN [8]  
 RP VARIANTS XSCID PHE-115; CYS-240 AND IL2-241.  
 RX MEDLINE=94130970; Pubmed=8299698;  
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,  
 RA de Saint Basile G.;  
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked  
 severe combined immunodeficiency disease result in the loss of  
 high-affinity IL-2 receptor binding.";  
 RL Eur. J. Immunol. 24:475-479(1994).  
 RN [9]  
 RP VARIANT XSCID LYS-68.  
 RX MEDLINE=94375038; Pubmed=8088810;  
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,  
 RA de Saint Basile G.;  
 RT "Detection of three nonsense mutations and one missense mutation in  
 the interleukin-2 receptor gamma chain gene in SCIDX1 that  
 differently affect the mRNA processing.";  
 RL Genomics 21:291-293(1994).  
 RN [10]  
 RP VARIANT XSCID HIS-162.  
 RX MEDLINE=94300093; Pubmed=8027558;  
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,  
 RA Kono T., Meda M., Uchiyama T., Sugamura K.;  
 RT "Impairment of ligand binding and growth signaling of mutant IL-2  
 receptor gamma-chains in patients with X-linked severe combined  
 immunodeficiency.";  
 RL J. Immunol. 153:1310-1317(1994).

RN [11]  
 RP VARIANT XSCID ASN-39.  
 RX MEDLINE=95023932; Pubmed=7937790;  
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,  
 RA de Saint Basile G.;  
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X  
 chromosome-linked severe combined immunodeficiency with peripheral T  
 cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).  
 RN [12]  
 RP VARIANTS XSCID CYS-226 AND HIS-226.  
 RX MEDLINE=95397841; Pubmed=7668284;  
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;  
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain  
 gene causing human X-linked severe combined immunodeficiency.";  
 RL Am. J. Hum. Genet. 57:564-571(1995).  
 RN [13]  
 RP VARIANT XSCID SER-183.  
 RX MEDLINE=96013903; Pubmed=7557965;  
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,  
 RA Levinsky R.L., Kinon C.;  
 RT "Screening for mutations causing X-linked severe combined  
 immunodeficiency in the IL-2R gamma chain gene by single-strand  
 conformation polymorphism analysis.";  
 RL Hum. Genet. 96:427-432(1995).  
 RN [14]  
 RP VARIANT XSCID 235-GLN--TRP-237 DUPL.  
 RX MEDLINE=95164726; Pubmed=7860773;  
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;  
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor  
 gamma-chain mutation causing X-linked severe combined  
 immunodeficiency.";  
 RL J. Clin. Invest. 95:895-899(1995).  
 RN [15]  
 RP VARIANT XSCID GLN-293.  
 RX MEDLINE=95190013; Pubmed=7883965;  
 RA Schmalstieg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E.,  
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;  
 RT "Missense mutation in exon 7 of the common gamma chain causes a  
 moderate form of X-linked combined immunodeficiency.";  
 RL J. Clin. Invest. 95:1169-1173(1995).  
 RN [16]  
 RP VARIANT XSCID ARG-115.  
 RX MEDLINE=97042245; Pubmed=8900089;  
 RA Stephan V., Mahn V., Le Dist F., Dirksen U., Broeker B.,  
 RA Mueller-Fleckenstein I., Horneft G., Schroten H., Fischer A.,  
 RA de Saint Basile G.;  
 RT "Atypical X-linked severe combined immunodeficiency due to possible  
 spontaneous reversion of the genetic defect in T cells.";  
 RL New Engl. J. Med. 335:1563-1567(1996).  
 RN [17]  
 RP VARIANT XSCID GLN-285.  
 RX MEDLINE=97295088; Pubmed=9150740;  
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,  
 RA Cant A., Kinon C.;  
 RT "B-cell-negative severe combined immunodeficiency associated with a  
 common gamma chain mutation.";  
 RL Hum. Genet. 99:677-680(1997).  
 RN [18]  
 RP VARIANT XSCID CYS-222.  
 RX MEDLINE=98064061; Pubmed=9399950;  
 RA Sharfe N., Shahar M., Rolfman C.M.;  
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus  
 morphology.";  
 RL J. Clin. Invest. 100:3036-3043(1997).  
 RN [19]  
 RP FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF  
 INTERLEUKINS.  
 CC -I- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7, IL-21  
 AND PROBABLY ALSO THE IL-13 RECEPTORS.  
 CC -I- SUBCELLULAR LOCATION: TYPE I membrane protein.  
 CC -I- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED  
 IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMAGLOBULINEMIA, SWISS TYPE  
 OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).

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CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD132 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".
CC -1- DATABASE: NAME=IL2Rbase; NOTE=X-linked SCID mutation database;
CC WWW="http://www.nhgri.nih.gov/DIR/GBR/SCID/".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D11086; BAA01857.1; -
DR EMBL: L12183; AAA59145.1; -
DR EMBL: L12178; AAA59145.1; JOINED.
DR EMBL: L12176; AAA59145.1; JOINED.
DR EMBL: L12177; AAA59145.1; JOINED.
DR EMBL: L12179; AAA59145.1; JOINED.
DR EMBL: L12180; AAA59145.1; JOINED.
DR EMBL: L12181; AAA59145.1; JOINED.
DR EMBL: L12182; AAA59145.1; JOINED.
DR EMBL: L19546; AAC37524.1; -
DR PIR: A42565; A42565.
DR PDB: 1ILM; 26-JAN-95.
DR PDB: 1ILN; 26-JAN-95.
DR Genew: HGNC:6010; IL2RG.
DR MIM: 308380; -
DR MIM: 300400; -
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.

* Query Match 10.5%; Score 220; DB 1; Length 369;
Best Local Similarity 25.5%; Pred. No. 7.5e-11;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

QY 97 LNKGEAKIHILFLPQCTNSE-VQSSMAETTYWISPOGIPETKVQDMDCVYNNMOYLIC 155
- - - - -
DB 19 LGVLTNTLITL-----PNGNEDFTADFLITMTDLSLSTLPLPVQCFVNEVEMNC 72
- - - - -
QY 156 SW-----KRGIVLDTNNLFLFYEGLDH--ALQCVDTIKADGQNGCAFFPLEASDY 207
- - - - -
DB 73 TWNSSSEPP-----TNTLHYKYNNSDNDKVKQSHYLFSEITSGCOLQKKEIHLX 125
- - - - -
QY 208 KDFICVNGSSENKPIRSSYFTFOLNIIVKPLPVVLTFTRESSCEIKLKWSTPLGP 267
- - - - -
DB 126 QTFVVOLODPRE--PRQATOMLKLQNDVLPWAPENLTLLKLSQLELMNN---NRF 180
- - - - -
DB 268 RCFDYIEIRED-DTTLVTAIVE-NETVTLKTNETRQLCFVVRKSNVNYICSDDGIMSEW 325
- - - - -
DB 181 HCLEHLVOYRTDMDSMTEDGSVDYRHKFSLPVSDGQKRYTFRVRSRNPPLCGSAQHMSSEW 240
- - - - -
QY 326 SDRQCEGSDLSKRTLLRFWLPFGFILLVYFTG 360
- - - - -
DB 241 SHPIHW-GSNTSKEN-----PFLALEAVVISVG 268
- - - - -

RESULT 9
PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=9932;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;
RX MEDLINE=94283267; Pubmed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning", expression, and mutational analysis of the pigeon prolactin
RT receptor.";
RL Endocrinology 135:269-276(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U07694; AAA20646.1; -
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hemopoetln_L_F1.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 4.
DR PROSITE: PS01352; HEMATOPO_RCL_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 133 263
FT CARBOHYD 263 263
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FT CARBOHYD 336 336
SQ SEQUENCE 830 AA; 94507 MW; 3B074E83CDE69EEF CRC64;

Query Match 10.3%; Score 216.5; DB 1; Length 830;
Best Local Similarity 24.4%; Pred. No. 3.9e-10;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

QY 18 TTEGCTSSDTEIKVNPDPDEIVDPGLS-----YVILQW 53
- - - - -
DB 97 TTYNITVMAANEIGSNS-----DPQYVDVTSTVQDPADVNLSTETKTSASTTYLLAKW 150
- - - - -
QY 54 QPPLSLDHFKECTV-EYELKYRNIGSEFTWKTITTKNLHYVGDGLNKGLAKIHTLLPWQ 112
- - - - -
DB 151 SPPPLADVTSNSHYRYELRLKPEKEKEMTV---SVGVOTQYKVN-LDAGVKYVVQVR 206
- - - - -
QY 113 CTNGSEVQSSMAETTYNISPG--IPETKVQDMDCVYNNMOYLICSKMRPGVLLDTNNYL 171
- - - - -
DB 207 CVLIDGEMSESSRRHINHGESPPEKPTTIKCRSEPKETTCWMPKPGSDGHPNTNYTL 266
- - - - -
QY 172 FYWYEGDLHALQVDYKADGQNGCFRPLASDYKDFICVNGSSENKPIRSSYFTFQ 231
- - - - -
DB 267 LYSKEGSEERYECPDY-KTAGPN-SCYFDKKNHSFWIITVYKATNEIGSNVSDPLYVD 324
- - - - -
QY 232 LQNIIVKPLPVVLTFTRESSCEIK---LKWS-IPLGP 284
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Db      325 VTIVQDPVPNVTLELKKTVNRKPYLVFTWSPPLADVRSGWLTLDYELRLKPEEA--- 381
Oy      285 TATVENEYITKTINERFOLCFVY-----RSKVNIYCSD--GINSWS-DKQCMWEGELS 337
Db      382 -----EEMETTFVQOQHMKFSLNPKKRYIVQIHKDPDHGHSWSESLERYLOIPTDFR 436
Oy      338 KKTLLRFLPFGFILLIVIFV 358
Db      437 IKDMY-VWITGVLSLICTLV 456

RESULT 10
CYRG_MOUSE
ID      CYRG_MOUSE      STANDARD:      PRT:      369 AA.
AC      P34902;
DT      01-FEB-1994 (Rel. 28, Created)
        01-FEB-1994 (Rel. 28, Last sequence update)
        15-JUN-2002 (Rel. 41, Last annotation update)
        Cytokine receptor common gamma chain precursor (Gamma-C)
        (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
DE      IL2RG.
        Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93277575; PubMed=8503926;
RA      Kunaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT      "Cloning of the mouse interleukin 2 receptor gamma chain:
        demonstration of functional differences between the mouse and human
        receptors.";
RL      Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CBA/CA;
RX      MEDLINE=93391374; PubMed=8378320;
RA      Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT      "Characterization of cDNAs encoding the murine interleukin 2 receptor
        (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
        Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93366191; PubMed=8359699;
RA      Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT      "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
        gamma.";
RL      Gene 130:303-304(1993).
RN      [4]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95104285; PubMed=7805729;
RA      Disanio J.P., Certain S., Wilson A., MacDonald H.R., Avner P.,
        Fischer A., de Saint Basile G.;
RT      "The murine interleukin-2 receptor gamma chain gene: organization,
        chromosomal localization and expression in the adult thymus.";
RL      Eur. J. Immunol. 24:3014-3018(1994).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=B6.S;
RX      MEDLINE=96341745; PubMed=8750189;
RA      Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
        Dougherty G.D.;
RT      "Molecular mechanisms regulating the hyaluronan binding activity of
        the adhesion protein CD44.";
RL      J. Neurooncol. 26:231-239(1995).
CC      -I- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
        INTERLEUKINS.
CC      -I- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7, IL-21
        AND PROBABLY ALSO THE IL-13 RECEPTORS.
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

```

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CC      -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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        or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: D13821; BAA02974.1; -.
DR      EMBL: U21795; AAA64279.1; -.
DR      EMBL: D13565; BAA02760.1; -.
DR      EMBL: L20048; AAA39286.1; -.
DR      EMBL: S75852; AAB32904.1; -.
DR      EMBL: S75844; AAB32904.1; JOINED.
DR      EMBL: S75845; AAB32904.1; JOINED.
DR      EMBL: S75847; AAB32904.1; JOINED.
DR      EMBL: S75848; AAB32904.1; JOINED.
DR      EMBL: S75849; AAB32904.1; JOINED.
DR      EMBL: S75850; AAB32904.1; JOINED.
DR      EMBL: S75851; AAB32904.1; JOINED.
DR      EMBL: X75337; CAA53085.1; -.
DR      PIR: JN0592; JN0592.
DR      PIR: JN0775; JN0775.
DR      HSSP: P31785; IILM.
DR      MGD: MGI:96551; IL2rg.
DR      InterPro: IPR002996; CR1A.
DR      InterPro: IPR003961; FN.III.
DR      Pfam: PF00041; fn3; 1.
DR      SMART: SM00060; FN3; 1.
DR      PROSITE: PS01355; HEMATOPO_REC_S_FL; 1.
KW      Receptor; Transmembrane; Glycoprotein; Signal.
FT      SIGNAL 1 22
FT      CHAIN 23 369
FT      DOMAIN 23 263
FT      TRANSMEM 264 284
FT      DOMAIN 285 369
FT      DOMAIN 151 250
FT      DISULFD 62 72
FT      DISULFD 102 115
FT      CARBOHYD 71 71
FT      CARBOHYD 75 75
FT      CARBOHYD 84 84
FT      CARBOHYD 96 96
FT      CARBOHYD 159 159
FT      CARBOHYD 164 164
SQ      SEQUENCE 369 AA; 42241 MW; CB2D5AB459077ACT CRC64;

Query Match 10.1%; Score 212.5; DB 1; Length 369;
Best Local Similarity 26.9%; Pred. No. 3.1e-10;
Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

Oy      136 PETKQDMDCVYNNQYLCSW----KPGIGVLDNTNLFYVYGLDHAL--QCVDYIK 189
Db      53 PTLPLPEVQCFYFNIEYNNCTNNSSEPOA-----TNLHRYKVSNNNTFQESHLTF 107
Oy      190 ADGQNGCRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIIVKPLPVYITFRE 249
Db      108 SKRITSQCIQKEDIQLQVTFVQL--DDPKRQRAVQKLMQLNVLIPRAVENTLISNL 165
Oy      250 SSCCEIKLWKSIPGLPIRACPFYELEIRD--DTLLVTAVNE--TYTLKTNETFOLCFV 307
Db      166 SESQLELRWK--SRHKKECLOLVQYKSNRSTWELIVNEPRSLPSVDELKRYIFR 223
Oy      308 VSKNIYICSDGINSWSDKQCMWG-----EDISKRTLRFWLPFGF--ILLIVFVYGL 361
Db      224 VSRNRNPLIGSSQQWSKMSQPVHMGSHYVENRPSLFALEAVLIPGTMLITLTFVYCW 283
Oy      362 LLRKPNYTP 370
Db      284 LRRMPPIP 292

```

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RESULT 11
CYRG_CANFA
ID CYRG_CANFA STANDARD: PRT: 373 AA.
AC P40321:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common gamma chain precursor (gamma-c)
DE Interleukin-2 receptor gamma chain (IL-2R gamma chain) (P64).
GN IL2RG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=9510114; PubMed=7829104;
RA Henthorn P.S., Somberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
RA Felsburg P.J.;
RA "IL-2R gamma gene microdeletion demonstrates that canine X-linked
RA severe combined immunodeficiency is a homologue of the human
RA disease.";
RT Genomics 23:69-74(1994).
RL -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7, IL-21
CC AND PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL: U04361; AAC48403.1; -.
CC HSSP: P31785; IILM.
CC DR InterPro: IPR002996; CRIA.
CC DR InterPro: IPR003961; FN.III.
CC DR InterPro: IPR003531; Hemtopoptn_S_F1.
CC SMART: SM00060; FN3; 1.
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
CC Receptor: Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 373 POTENTIAL.
FT DOMAIN 23 261 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT TRANSMEM 262 283 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 284 373 POTENTIAL.
FT DOMAIN 151 249 CYTOPLASMIC (POTENTIAL).
FT DISULFID 62 72 FIBRONECTIN TYPE-III.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SQUONCE 373 AA; 42516 MW; 03A0DEFB80898B CRC64;

Query Match 9.9%; Score 208; DB 1; Length 373;
Best Local Similarity 26.0%; Pred. No. 7.4e-10;
Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

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QY 115 NGSE-----VOSSMAETTYWISPGIPEYKQVODMDCVYYNMWOLICSW-----KPGI 161
DQ 31 NGNEDIIPDEFPLATPSET---LSVSSILPLEVO---CFVFNVEYMNCTNMSSESRP-- 82
QY 162 GVLDDTYNINLEFYWEGL--DHALQCVDIYKADGNCNICRPPYLEASDYKPFYICVNSSE 219
DQ 83 -----TNULTLHYWYKNSNDKRVQCGHYLFESREVTACWMLQKEIHLIYEFVQALRDPRE 137
QY 220 NKPIRSSYFETOLQNIYKPLPPVYLFTRESCEIKLKWSIPLGIPARCFDEYEIRED 279
DQ 138 --PRKSTQKLIKQNLQNIYIPAPENULTIHLNSESQLELSWS---NRHLDCLEHYVQYRSD 192
QY 280 -DTTLVTATVEN-ETTYLKTTNETRQLCFYVRKSNVNYCSDDGIMSEWSDKQCEGEDLS 337
DQ 193 WDRSWTQSDVDRHNSFSLPSVDGKFYTFPRVRSRYNPLCGSAQMSWSHPIMH-GSNTS 251
QY 338 KKTLL-----RFWLPRGFILILVIFV 358
DQ 252 KENPLFASEAVLIPLGSMGLIISLI 276

RESULT 12
IL3B_MOUSE
ID IL3B_MOUSE STANDARD: PRT: 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-3 receptor class II beta chain precursor (colony
DE stimulating factor 2 receptor, beta 2 chain).
GN CSF2RB2 OR AIZCA OR IL3RB2 OR IL3R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90117145; PubMed=2404337;
RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
RA Ybarga I., Arai K., Miyajima A.;
RT Cloning of an interleukin-3 receptor gene: a member of a distinct
RT receptor gene family.
RL Science 247:324-327(1990).
RL -1- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3
CC RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
CC OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5
CC AND GM-CSF RECEPTORS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL: M28855; AAA39295.1; -.
CC PIR: A40091; A40091.
CC DR MGI:1339760; Csf2rb2.
CC DR InterPro: IPR002996; CRIA.
CC DR InterPro: IPR000282; Cytok receptor_2.
CC DR InterPro: IPR003961; FN.III.
CC DR InterPro: IPR003531; Hemtopoptn_S_F1.
CC PIRam: PF00041; FN3; 2.
CC SMART: SM00060; FN3; 2.
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
CC Receptor: Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 878 INTERLEUKIN-3 RECEPTOR CLASS II BETA
FT CHAIN CHAIN.

```

FT	DOMAIN	23	440	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	441	462	POTENTIAL.
FT	DOMAIN	463	878	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	39	49	BY SIMILARITY.
FT	DISULFID	78	95	BY SIMILARITY.
FT	DISULFID	254	264	BY SIMILARITY.
FT	DISULFID	293	310	BY SIMILARITY.
FT	CARBOHYD	62	62	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	350	350	N-LINKED (GLCNAC. . .) (POTENTIAL)
SO	SEQUENCE	878 AA;	97195 MW;	B8BC9092ADDC24D56 CRC64;

Query Match	9.3%	Score 195;	DB 1;	Length 878;
Best Local Similarity	24.1%	Pred. No. 2.5e+08;		
Matches	86;	Conservative	150;	Indels 62;
		Mismatches	150;	Gaps 23

```

Oy 34 PRDFEIVDPGLGLYLQMOPL--SLDHFEKCYEYELKYNKISSEYKTIITNLH 90
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
139 PPKDHIHPSG--DHFLLEWSSVLGDSQVSWLSSKIDEEFVAYKRL-ODSWED--AASLH 193
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
91 YKDGFLDKKGIETKHTLLP-----WQGTNGSEVQ--SSMAETTYLISPGIPEI 138
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 194 -TSNQVN--LEPKL-FLPNSIYAARYRTLSAGSSISGSRPSKSPSEVHNDSPG-DKA 247
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 139 KYVDDECYUWMOYLKSCMRKPGIGVLLDTNYNLEFYWEGLDHALQCYDYLQAOQNI--- 195
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 248 QPQNIQCFDFDGIQSIHCSEWEMTQTSVSGLETTYRSPRAPEKCSVPVAKPEQASYYTR 307
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 196 -GCRPYLEASDYKDFEYLCVANGSSSENKRINSYTFPQNIYKPELPVY-LTYRESSECE 253
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 308 YRCSLPVPERPSAHQYTVSVKHLQKRT-MSYHIQME-----PRLNGTKNRDS--- 357
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 254 IKLKMSITGLPRAPCFD--YEIETREDDTLVATYEN---ETYLKTTNETRQLCEV 307
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 358 YSLHMETOKIP---KYIDHTFOVOYKKKSEWSKSKSTENLGRVSMDLPOLEPDTSYCAR 414
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 308 VRSK-VNLYCSDDGIWSEMSKOCMEGBDLSKTLRLRMYLPEFGLILIVFYVGLL 363
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 415 VAVKATISDY---DGIWSEMSENYWT-NDWMPYL--WT---VLIIVELIFPTLL 460
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

	RESULT	13
CYRG_BOVIN	STANDARD;	PRT: 379 AA.
ID	095118;	
AC	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
	Cytokine receptor common gamma chain precursor (Gamma-C)	
	(Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (p64)	

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96268473; PubMed=8672241;  
RA Yoo J., Stone R. T., Solinas-Roldo S., Fries R., Beattie C.W.;  
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor  
gamma gene.";  
RL DNA Cell Biol. 15:453-459(1996).  
CC -I- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF  
CC INTERLEUKINS.  
CC  
CC -I- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7, IL-21  
CC AND PROBABLY ALSO THE IL-13 RECEPTORS.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
CC  
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DR EXBL; U33748; AAB07812.1; -.  
DR HSP; P31785; IIM.  
DR InterPro: IPR002996; CRA.  
DR InterPro: IPR003361; FN\_III.  
DR InterPro: IPR003331; Hemtopoptn\_S\_F1  
Name: PR00041; 533-1

DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01355; HEMATOPO\_REC\_S\_F1; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal  
CSTMT 1 DOMESTIC 33

FT	CHAIN	23	379		CYTOKINE RECEPTOR COMMON GAMMA CHAIN
FT	DOMAIN	23	269		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	270	290		POTENTIAL.
FT	DOMAIN	291	379		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	158	256		FIBONECTIN TYPE-III.
FT	DISULFID	68	78		POTENTIAL.
FT	DISULFID	109	122		POTENTIAL.
FT	CARBOHYD	77	77		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	81	81		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	90	90		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	166	166		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	171	171		N-LINKED (GLCNAC. . .) (POTENTIAL).
50	SEQUENCE	379 AA:	43037 MW:		33CEAD90CB032178 CRC64:

Query Match	9.0%	Score 189.5	DB 1	Length 379
Best Local Similarity	26.2%	Pred NO. 2.5e+08		
Matches 62, Conservative	42	Mismatches 106	Indels 27	Gaps 9

```

QY 135 IPETKYQDMCVYNNMOYLCSW-----KRGIGVLDTNNTLFWY---EGDLHALQCV 168
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 LPLPVGQ--CFEYVWEYMCNTMNSSSEPQ-----NNLTLLHYGYRNGDKDLQECG 110
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 186 DYKADGQNICRPFYLEASDYKDPFYLCVNSSSENKPIRSYFFPOLONTYKPLPYVLT 245
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 111 HLYSEGTSCSWPKEKIRLYETFFVOLQDPREHR--KQPKMLKIQDULVAPANLTL 168
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 246 FTRESSECIKLSWIPGLPIPARCFDEVEIRED-DFTLVATVEN--EYTLKLTNETRQ 303
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 169 LKRNSEFQLEIWSM---NRYDLCHLEHLYQYRSDRNSMTWQSDYDHKHSLSLSPVDQKL 225
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Qy 304 LCFVVRSKVNITCSDDGIWSEWSDKQCWEGBDSLKTKLLREWFPGFIIILVIIVTG 360  
| | | | | : | : | : |  
Db 226 YTFRRRSRYNPLCGSAQHMSDWSPYTHW-GSNTSKENIENPENPSLFALEAVLLPLG 281

RT	RESULT 14		
RT	CYRB_HUMAN		
AC	P32927	STANDARD;	PRT; 897 AA.
DT	01-OCT-1993 (Rel. 27, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Cyclokinine receptor common beta chain precursor (CDw131 antigen) .		
GN	CSF2RB OR IL5RB OR IL3RB.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91088571; PubMed=1702217;		
RA	Hayashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,		
RA	Miyajima A.;		
RT	"Molecular cloning of a second subunit of the receptor for human		
RT	granulocyte-macrophage colony-stimulating factor (GM-CSF):		
RT	reconstitution of a high-affinity GM-CSF receptor.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).		
RT	[2]		

RA REVISION TO 454.

RL Klamura T.;

CC Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5

CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.

CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA

CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw31 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw31.htm".

CC

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CC

DR EMBL: M59941; AAA18171.1; -

DR PIR: A39255; A39255.

DR HSSP: P19235; 1EBA.

DR Genew: HGNC:2436; CSF2RB.

DR MIM: 138981; -

DR InterPro: IPR002996; CRA1.

DR InterPro: IPR000282; CYTOK\_receptor\_2.

DR InterPro: IPR003961; FN.III.

DR InterPro: IPR003531; Hemtopoptn\_S.F1.

DR Pfam: PF00041; fn3; 2.

DR SMART: SM00060; FN3; 2.

DR PROSITE: PS01355; HEMAPOPO\_REC\_S.F1; 1.

DR KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 897 CYTOKINE RECEPTOR COMMON BETA CHAIN.

FT DOMAIN 17 443 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 444 460 POTENTIAL.

FT DOMAIN 461 897 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 129 238 FIBRONECTIN TYPE-III 1.

FT DOMAIN 336 434 FIBRONECTIN TYPE-III 2.

FT DISULFD 35 45 BY SIMILARITY.

FT DISULFD 75 91 BY SIMILARITY.

FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 897 AA; 97335 MW; 3398B3F7DB8F93A CRC64;

Query Match 8.5%; Score 178.5; DB 1; Length 897;

Best Local Similarity 22.5%; Pred. No. 5.8e-07;

Matches 89; Conservative 57; Mismatches 144; Indels 105; Gaps 21.

0Y 32 VNPDPFEIVDPGYGY-----LYLQWQP-----LSIDHF----- 62

Db 97 VIPCSFVVTVTDVDFSPDPDRPLRTLVTLVTLQHQAPPEPRDLQISTODDHFLLTWSVAL 156

0Y 63 -----KECVKEELKYNRNGSETWK--TIITKLNHKKOSFDLKKGIE-----A 103

Db 157 GSPQSHMLSPGDLLEEVYVKRL-QDSWEAALLLSNTS-----QATLGEHMLPSSTYYA 210

0Y 104 KIH-T-LPPOCTNGSEVOSMAETTYTWISPOGIEPTKQYODMDCVYVNMQYLLCSMKPGIG 162

Db 211 RVRTRLAGSRISGR--PSKMSPEVCWMSQPE-DEAQPNLNECFPDGAVALVSCMSVEVKE 267

0Y 163 VLDLTNYLFTWYEEGLDALQCVDIKADGQNG-----CRPFYLEASDYKDFYICVN 215

Db 268 VASSVSEFLFKRPSDAGEEESCPLAR--EGIGSLHTRHHOICIVPDPATRGQYIVSYQ 324

0Y 216 GSSEKKPRRSSTFRTQLOINYKRLPVYLLTFPSSCEIKLWSIPLGIPARCDYEIE 275

Db 325 PRRAEKHKSSV-----NI-QAMPSPSLNTYKKDD-SYSLWELWETMKKRYEIIIDTFEIO 375

0Y 276 IREDDTLVLTAT-VENEYTYLTKTN-----ETROLCLFV-VRSKVNIVYCSDDGIMSE 324

[illegible]

```
Db 94 CVPKRCVPIPY---TRFSITNEDYYSFRPDSDLGIQLMWPLAQNVOPLPKNVSISSSEDR 150
QY 49 LYIQWQPPPL---SLDHEKCEIVEYEIKRNIGSETWKTITTKN-----LHKDGFDLNKG 100
Db 151 FLEMSVSLGDAQVSWLSSKDIEFEVAYKRL-ODSWEDAYSLHTSKFQVNEPEPKLFLPNS 209
QY 101 IEA-KIHT-ILPMQCTNGSEVOSSMAETTYWISPOGIPETKVODMDCVYNNQYLLCSMK 158
Db 210 IYAPRVRTRLYPGSSLSGR--PSRKSPEAHWDSPG-DKAQPONLQCFDGIQSLHCSWE 266
QY 159 PGIGVLLDPNNLFFYWEGLDHALQCVDIK-ADGQNI---GCRFPYLEASDYKDFYIC 213
Db 267 VMTQTTGSVSFGLFYRPSVAPBEKCSPVKPEPGASVYTRYHCSLPVPEPSAHSQYTVS 326
QY 214 VNGSSEKPIRSSYFTFOLQNIIVKPLPPVYLTFTRESSCEIKLWSIPLGPIPARCFDYE 273
327 V-----KHLBOGKFIMSYNHIOHEPPTLNLTKNRDS---YSLHWETOKMAYSFIEHTFQ 377
274 IEIREDPTTLVTAIVEN--ETYTLLKTNETRQLCFVVRSKVNIYCSDDGIWSEMSDKQW 331
Db 378 VOYKKKSDSWEDSKTENIDRAHSMDSQLEPDTSYCARVRVKPISNYDGIMSKWSEETW 437
QY 332 EGEDLSKRTLLRFWLPFGFILLIVFYTGILL 363
Db 438 K-TDWMVMPYL--WI---VLIVFLILITLLL 461
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Search completed: January 24, 2003, 19:36:39  
job time : 17 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:31:49 ; Search time 37 Seconds

(without alignments)  
1368.520 Million cell updates/sec

Title: US-09-714-792a-4

Perfect score: 2104

Sequence: 1 MAFVCLAIICLYFLISTTF.....LLLRKPNTYPKMIPFECDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A\_Geneseq\_101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	100.0	380	18	AAW24972 Human interleukin-
2	2104	100.0	380	18	AAW35295 Human IL-13 bindin
3	2104	100.0	380	18	AAW36613 Human zcytor2 cyto
4	2104	100.0	380	19	AAW41520 Human HR-1 recepto
5	2104	100.0	380	19	AAW41502 Human cytokine/pep
6	2104	100.0	380	19	AAW33603 Homo sapiens HR-1
7	2104	100.0	380	21	AAW95296 IL-13 binding chai
8	2104	100.0	380	22	AAW63812 Amino acid sequenc
9	2104	100.0	380	22	AAW72136 Human interleukin
10	2104	100.0	380	22	AAW29748 Human IL-13 recept

11	2104	100.0	380	23	AAW49201 Human IL-13R alpha
12	2078	98.8	380	18	AAW36614 Human zcytor2 cyto
13	1853	88.1	372	18	AAW36616 Celebous macaque zc
14	1764	83.8	317	23	AAE13746 Human soluble cyto
15	1753	83.3	315	19	AAW56261 Mature interleukin
16	1753	83.3	359	19	AAW56260 Construct containi
17	1503	71.4	386	22	AAW69135 Canine interleukin
18	1452.5	69.0	355	22	AAW69136 Canine interleukin
19	1392.5	66.2	318	22	AAW69137 Canine IL-13R exte
20	1382.5	66.2	561	22	AAW69138 Canine IL-13Ralph
21	1392.5	66.2	561	22	AAW69141 Canine IL-13Ralph
22	1392.5	66.2	563	22	AAW69140 Canine IL-13Ralph
23	1392.5	66.2	565	22	AAW69139 Canine IL-13Ralph
24	1194.5	56.8	383	21	AAW35294 Murine IL-13 bindi
25	1194.5	56.8	383	21	AAW35295 Murine IL-13 bindi
26	1194.5	56.8	383	22	AAW72135 Murine interleukin
27	1194.5	56.8	383	22	AAW29747 Mouse IL-13 recept
28	935.5	44.5	255	22	AAW69134 Canine interleukin
29	626.5	29.8	145	22	AAW69133 Canine interleukin
30	456	21.7	157	19	AAW56252 Interleukin-13 bin
31	311.5	14.8	366	13	AAW22216 Sequence of human
32	311.5	14.8	366	13	AAW22220 Sequence of secret
33	311.5	14.8	420	13	AAW22219 Sequence of secret
34	311.5	14.8	420	19	AAW82842 Human interleukin-
35	310.5	14.8	421	13	AAW25064 Human IL-5 recepto
36	305.5	14.5	420	13	AAW22215 Sequence of human
37	302.5	14.4	405	22	AAW69132 Canine interleukin
38	297	14.1	313	18	AAW21856 Protein used in pr
39	296	14.1	426	18	AAW09821 Mouse interleukin-
40	295.5	14.0	427	18	AAW24973 Human interleukin-
41	295.5	14.0	427	22	AAW19807 Human interleukin-
42	294.5	14.0	426	18	AAW09822 Human interleukin-
43	292.5	13.9	1026	16	AAW70121 IL5-R-GDP 130 fusi
44	292	13.9	335	13	AAW25063 Soluble human IL-5
45	292	13.9	335	14	AAW33699 shIL-5R-alpha. Sy

#### ALIGNMENTS

RESULT 1	
AAW24972	AAW24972 standard; protein; 380 AA.
XX	XX
AC	AAW24972:
XX	XX
DT	22-JUN-1998 (first entry)
XX	XX
DE	Human interleukin-13 beta receptor.
XX	XX
KW	Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
XX	XX
OS	Homo sapiens.
XX	XX
PN	W09720926-A1.
XX	XX
PD	12-JUN-1997.
XX	XX
PF	07-NOV-1996; 96WO-FR01756.
XX	XX
PR	06-DEC-1995; 95FR-0014424.
XX	XX
PA	(SNFI) SANOFI SA.
XX	XX
PI	Caput D, Ferrara P, Laurent P, Vltá N;
XX	XX
DR	WPI: 1997-319773/29.
XX	XX
DR	N-PSDB; AAT85826, AAT86464.
XX	XX
PT	New purified human interleukin-13 receptors - and related nucleic
PT	acids, useful for diagnosis and treatment of inflammation, allergy,
PT	etc

PS Claim 1; Figure 2a; 83pp; French.  
XX  
CC This sequence represents interleukin-13 (IL-13) beta receptor. The  
CC invention relates to new purified peptides comprising 380 or 427 amino  
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
CC affinity, but acquires high affinity when associated with the IL-4  
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as  
CC diagnostic probes to identify aberrant synthesis or genetic anomalies  
CC such as loss of heterozygosity and rearrangements, or chromosomal  
CC anomalies. They are also used for production of recombinant IL-13R beta  
CC and alpha which can be used as IL-13 antagonists, specifically to  
CC regulate IL-13-induced responses for treatment of inflammation and  
CC allergy. IL-13 receptors are also useful as antisense molecules for gene  
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard  
CC immunoassays) to diagnose diseases associated with abnormal expression  
CC of IL-13 receptors; when coupled to a toxin also for treatment of  
CC overproduction of IL-13R. Cells that express IL-13R at the surface are  
CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta  
CC is encoded by the nucleic acid sequence shown in Figure 2a in the  
CC specification (AAT86464), which is not the same as that shown in the  
CC sequence listing (AAT85828).

XX Sequence 380 AA:

Query Match 100.0%; Score 2104; DB 18; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPLSLD 60  
DB 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPLSLD 60  
OY 61 HFKCTVEYELKRYNIGSEFWKTIITNKLHYKDGFDLNKGEAKIHLLPWOCTNSEVQ 120  
DB 61 HFKCTVEYELKRYNIGSEFWKTIITNKLHYKDGFDLNKGEAKIHLLPWOCTNSEVQ 120  
OY 121 SSMAETTYWISPOGIPETKVDMDCVYNNQYLLCSMKPGIGVLLDNTNLYFWYEGLDH 180  
DB 121 SSMAETTYWISPOGIPETKVDMDCVYNNQYLLCSMKPGIGVLLDNTNLYFWYEGLDH 180  
OY 181 ALOCVDYIKADGONIGCRFPYLEASDYKDRFYICVNGSSENKPIRSSYFTFOLQNIKPLP 240  
DB 181 ALOCVDYIKADGONIGCRFPYLEASDYKDRFYICVNGSSENKPIRSSYFTFOLQNIKPLP 240  
OY 241 PVIYLTFTRESSCEIKLKWSPILGPIPARCFDEYIEIREDDTTLTAVENETYLKTTNE 300  
DB 241 PVIYLTFTRESSCEIKLKWSPILGPIPARCFDEYIEIREDDTTLTAVENETYLKTTNE 300  
OY 301 TROLCFVVRSKVNITYCSDDGIMSEMSDKQCEGDLTKTLRFLPFGFTLLIVFVTG 360  
DB 301 TROLCFVVRSKVNITYCSDDGIMSEMSDKQCEGDLTKTLRFLPFGFTLLIVFVTG 360  
OY 361 LLRKRPNTYPRMIDPEFCDT 380  
DB 361 LLRKRPNTYPRMIDPEFCDT 380

RESULT 2  
AAM35295  
ID AAM35295 standard; Protein: 380 AA.  
XX  
AC AAM35295;  
XX  
DT 27-MAR-1998 (first entry)  
XX  
DE Human IL-13 binding chain of the IL-13 receptor.  
XX  
KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;  
KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;  
KW allergy; asthma; immune complex disorder.  
XX  
..-3

OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..25 /label= signal\_sequence  
FT Protein 26..380 /note= "putative"  
FT Domain 26..341 /label= mature\_protein  
FT Domain 342..362 /label= extracellular\_domain  
FT Domain 363..380 /label= transmembrane\_domain  
FT Domain /label= intracellular\_domain  
PN W09731946-A1.  
PD 04-SEP-1997.  
XX  
XX 28-FEB-1997; 97WO-0503124.  
XX  
XX 01-MAR-1996; 96US-0609572.  
XX  
XX (GENY ) GENETICS INST INC.  
XX  
XX Collins M, Donaldson D, Filtz L, Neben T, Whilters M;  
PI Wood C;  
XX  
XX WPI; 1997-448632/41.  
DR N-PSDB; AAT95214.  
XX  
XX New nucleic acid encoding interleukin-13 receptor binding chain and  
PT transformed cells - proteins, antibodies and inhibitors, for  
PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
PT and in diagnosis  
XX  
PS Claim 11; Pages 34-35; 49pp; English.  
XX  
XX The present sequence represents the human interleukin-13 (IL-13) binding  
CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a  
CC mediator of the known biological activities of IL-13. Recombinant  
CC IL-13bc proteins, and antibodies raised against them, are used to  
CC inhibit the binding of IL-13 to its receptor. They are particularly used  
CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex  
CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.  
CC They are also used to treat immune deficiency (particularly in  
CC haematopoietic progenitor cells), cancer etc., and to increase macrophage  
CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  
CC with such activity is combined with IL-13bc and the mixture applied,  
CC in vivo, to a cell expressing at least one chain of the IL-13 receptor  
CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect  
CC expression of IL-13, its receptor or binding chain, and to raise specific  
CC antibodies which may be useful for treating some tumours.  
XX  
SQ Sequence 380 AA:

Query Match 100.0%; Score 2104; DB 18; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPLSLD 60  
DB 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPLSLD 60  
OY 61 HFKCTVEYELKRYNIGSEFWKTIITNKLHYKDGFDLNKGEAKIHLLPWOCTNSEVQ 120  
DB 61 HFKCTVEYELKRYNIGSEFWKTIITNKLHYKDGFDLNKGEAKIHLLPWOCTNSEVQ 120  
OY 121 SSMAETTYWISPOGIPETKVDMDCVYNNQYLLCSMKPGIGVLLDNTNLYFWYEGLDH 180  
DB 121 SSMAETTYWISPOGIPETKVDMDCVYNNQYLLCSMKPGIGVLLDNTNLYFWYEGLDH 180  
OY 181 ALOCVDYIKADGONIGCRFPYLEASDYKDRFYICVNGSSENKPIRSSYFTFOLQNIKPLP 240

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|||||
Db 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIYKPLP 240
QY 241 PVLTFTRSSCEIKLKWISIPGPIPARCFDYEIEIREDDTLVATVVENETYLKTNE 300
Db 241 PVLTFTRSSCEIKLKWISIPGPIPARCFDYEIEIREDDTLVATVVENETYLKTNE 300
QY 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVNG 360
Db 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVNG 360
QY 361 LLRRKPNITYPKMIPEFCDT 380
Db 361 LLRRKPNITYPKMIPEFCDT 380

RESULT 3
AAM36613
AAM36613 standard; Protein: 380 AA.
AC AAM36613;
DT 30-MAR-1998 (first entry)
XX Human zcytor2 cytokine receptor protein.
DE Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KM infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Domain 340..363
FT Domain /label= transmembrane_domain
FT Domain 364..380
FT Domain /label= intracellular_domain
FT Domain 25..339
FT Domain /label= ligand_binding_domain
XX
XX W09733913-A1.
XX 18-SEP-1997.
XX 12-MAR-1997; 97MO-US04043.
XX 13-MAR-1996; 96US-0013345.
XX (ZYMO ) ZYMOGENETICS INC.
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
XX O'hara FJ;
XX WPI: 1997-470820/43.
XX N-PSDB: AAT96782.
XX
XX New nucleic acid encoding testis-specific cytokine receptor - useful
XX for identification of ligands or antagonists, potentially for use as
XX male contraceptives or for infertility treatment
XX
XX Claim 2: Page 47-48; 79pp; English.
XX
XX This sequence represents a novel ligand-binding receptor, zcytor2,
XX which shares homology with cytokine receptors and was isolated from human
XX placental polyA+ RNA. The resulting polypeptide is a receptor for
XX cytokines (particularly interleukin-13) and is expressed on the surface
XX of testicular cells, probably being involved in spermatogenesis. It can
XX be used to detect ligands that promote proliferation and/or
XX differentiation of such cells in cultures and may also be used to treat
XX infertility. Antagonists of this receptor may be used to characterise
XX ligand-receptor interactions and as male-specific contraceptives. By
XX blocking the action of IL-13, receptor antagonists and ligand-binding
XX this receptor can also be used to modulate immune function, e.g. in
XX allergy and asthma, as a diagnostic to determine circulating levels of

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CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX
XX Sequence 380 AA;
XX
XX Query Match 100.0%; Score 2104; DB 18; Length 380;
XX Best Local Similarity 100.0%; Pred. No. 2e-197;
XX Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIQCLYTLFTLSTFGCTSSDPEIKVNPQDFEIVDPGLGYLYLOMOPPLSD 60
Db 1 MAFVCLAIQCLYTLFTLSTFGCTSSDPEIKVNPQDFEIVDPGLGYLYLOMOPPLSD 60
QY 61 HFECTVEYELKRYNIGSETWKTITKNIHYDGFDLNKGIAKIHILLPMQCTNGSEVQ 120
Db 61 HFECTVEYELKRYNIGSETWKTITKNIHYDGFDLNKGIAKIHILLPMQCTNGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVDMDCVYVNMQYLLCSMRKGIVLLDTNINLFYWEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVDMDCVYVNMQYLLCSMRKGIVLLDTNINLFYWEGLDH 180
QY 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIYKPLP 240
Db 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIYKPLP 240
QY 241 PVLTFTRSSCEIKLKWISIPGPIPARCFDYEIEIREDDTLVATVVENETYLKTNE 300
Db 241 PVLTFTRSSCEIKLKWISIPGPIPARCFDYEIEIREDDTLVATVVENETYLKTNE 300
QY 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVNG 360
Db 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVNG 360
QY 361 LLRRKPNITYPKMIPEFCDT 380
Db 361 LLRRKPNITYPKMIPEFCDT 380

RESULT 4
AAM41520
ID AAM41520 standard; Protein: 380 AA.
XX
XX AAM41520;
XX 22-JUN-1998 (first entry)
XX Human HR-1 receptor.
XX
XX HR-1 receptor; human; cytokine; infection; asthma; allergy;
XX haematopoietic disorder; tumour; therapy; diagnosis.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX Protein /label= Sig_peptide
XX Protein 22..380
XX Protein /label= Mat_protein
XX
XX W09747741-A1.
XX 18-DEC-1997.
XX 12-JUN-1996; 96MO-US10262.
XX 12-JUN-1996; 96MO-US10262.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Appelbaum ER, Hu J;

```

XX WP1: 1998-052308/05.  
 DR N-PSDB: AAV04131.  
 XX Nucleic acid sequence encoding human cytokine peptide hormone  
 PT receptor - useful to treat, prevent or diagnose, e.g. lowered  
 PT resistance to infection, asthma, allergy or haematopoietic disease  
 XX  
 PS Claim 13: Page 62-64: 76pp: English.  
 CC This protein comprises a novel human cytokine/peptide hormone  
 CC receptor, designated the HR-1 receptor, that shows 27% identity  
 CC and 52% similarity to the Interleukin-5 receptor. Its amino acid  
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a  
 CC human testis library. Recombinant HR-1 receptor can be expressed  
 CC in claimed host cells, and used in a claimed method for identifying  
 CC compounds which bind to, and activate or inhibit, it. HR-1  
 CC receptor activators and agonists can be used to treat, prevent or  
 CC diagnose predisposition to lowered resistance to infection, asthma,  
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,  
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.  
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can  
 CC be used to treat conditions associated with HR-1 receptor  
 CC overexpression. The antibodies can also be used to determine HR-1  
 CC receptor levels, since overexpression may be diagnostic of tumours.  
 CC  
 XX Sequence 380 AA:  
 Query Match 100.0%; Score 2104; DB 19; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 2e-197;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 QY 61 HFKECTVEYELKYNIGSETWKTITTKMLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 QB 61 HFKECTVEYELKYNIGSETWKTITTKMLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 QY 121 SSMATTYTWISPOGIPETKVDMDCVYNNMOYLCSMKPGIGVLDNTYNLFWYEGLDH 180  
 DB 121 SSMATTYTWISPOGIPETKVDMDCVYNNMOYLCSMKPGIGVLDNTYNLFWYEGLDH 180  
 QY 181 ALOCVDYIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLONIKPLP 240  
 DB 181 ALOCVDYIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLONIKPLP 240  
 QY 241 PYYLFTFTRESSCEIKLKWISIPGPIPARCFDEIREDDTLVATVENEETYLTKTNE 300  
 241 PYYLFTFTRESSCEIKLKWISIPGPIPARCFDEIREDDTLVATVENEETYLTKTNE 300  
 QY 301 TROLCFVVRSKVNYICSDGIMSEWSKQCGEGEDLSKKTLLRFLPFGFILLIVFVG 360  
 DB 301 TROLCFVVRSKVNYICSDGIMSEWSKQCGEGEDLSKKTLLRFLPFGFILLIVFVG 360  
 QY 361 LLRKRPNTYPKMIPEFCDF 380  
 DB 361 LLRKRPNTYPKMIPEFCDF 380

RESULT 5  
 ID AAM41502 standard: Protein: 380 AA.  
 XX AAM41502:  
 AC  
 XX  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Human cytokine/peptide receptor, HR-1 receptor.  
 XX  
 KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;  
 KW Infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;

KW neutropaenia; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT /label= sig\_peptide  
 FT Protein 22..380  
 FT /label= Mat\_protein  
 FT /note= "Claim 14"  
 XX  
 PM EP812913-A2.  
 XX  
 PD 17-DEC-1997.  
 XX  
 XX 04-JUN-1997; 97EP-0303815.  
 PR 12-JUN-1996; 96US-0017843.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Appelbaum ER, Hu J;  
 XX  
 DR WP1: 1998-034974/04.  
 DR N-PSDB: AAV04075.  
 XX  
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to  
 PT increase resistance to infections in individuals with trauma and/or  
 PT burns  
 PS  
 PS Claim 13: Page 27-28: 34pp: English.  
 CC This protein comprises a novel human cytokine/peptide hormone  
 CC receptor, designated HR-1 receptor. The amino acid sequence  
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human  
 CC testis cDNA library. It shows 27% amino acid identity and 52%  
 CC similarity with the human interleukin-5 receptor. Also claimed are  
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an  
 CC agonist to the polypeptide, antibody against the polypeptide, an  
 CC antagonist that inhibits the activity of the polypeptide, a process  
 CC for diagnosing a disease, or a susceptibility to disease, related  
 CC to expression of HR-1 receptor, and a method for identifying  
 CC compounds that activate or inhibit the HR-1 receptor. HR-1  
 CC receptor protein and polynucleotides can be used for research,  
 CC biological, diagnosis and (gene) therapy applications, e.g. to  
 CC increase resistance to infections in individuals with trauma and/or  
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine  
 CC predisposition to asthma, allergic disorders or disorders of  
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or  
 CC cyclic neutropaenia or as a consequence of cytotoxic therapy of  
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.  
 CC  
 XX Sequence 380 AA:  
 Query Match 100.0%; Score 2104; DB 19; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 2e-197;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 QY 61 HFKECTVEYELKYNIGSETWKTITTKMLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 DB 61 HFKECTVEYELKYNIGSETWKTITTKMLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 QY 121 SSMATTYTWISPOGIPETKVDMDCVYNNMOYLCSMKPGIGVLDNTYNLFWYEGLDH 180  
 DB 121 SSMATTYTWISPOGIPETKVDMDCVYNNMOYLCSMKPGIGVLDNTYNLFWYEGLDH 180  
 QY 181 ALOCVDYIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLONIKPLP 240  
 DB 181 ALOCVDYIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLONIKPLP 240

Db 181 ALOCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTPOLQNTVRLP 240  
 QY 241 PVLFTFRESSCEIKLKWISIPGPIPARCFDEIEIRDDDTTLVATVAVENETYLKTTNE 300  
 Db 241 PVLFTFRESSCEIKLKWISIPGPIPARCFDEIEIRDDDTTLVATVAVENETYLKTTNE 300  
 QY 301 TROLCEVVRKVNITYCSDGIMSEMSDKQCEGEDLSKRTLLRFLPRGFTLLIVIFVTG 360  
 Db 301 TROLCEVVRKVNITYCSDGIMSEMSDKQCEGEDLSKRTLLRFLPRGFTLLIVIFVTG 360  
 QY 361 LLKRPNTPYRKMIPEFCDT 380  
 Db 361 LLKRPNTPYRKMIPEFCDT 380  
 RESULT 6  
 AAM33603  
 AAM33603 standard; Protein: 380 AA.  
 AAM33603:  
 XX 08-JUN-1998 (first entry)  
 DT XX Homo sapiens HR-1 receptor.  
 DE XX  
 XX Cytokine; hormone receptor; AIDS; acquired immune deficiency;  
 KM syndrome; aplastic anaemia; neutropenia; cancer treatment;  
 KM infection resistance; diagnosis; tumours; HR-1 receptor;  
 KW asthma; allergic; haematopoietic; disorder.  
 XX Homo sapiens.  
 40S XX  
 FH Key  
 FT Peptide 1..21 location/Qualifiers  
 2, FT /note= "signal peptide"  
 XX  
 XX WO9747742-A1.  
 PN 18-DEC-1997.  
 PD XX  
 XX 09-JUL-1996; 96WO-US11459.  
 PF XX  
 XX 12-JUN-1996; 96WO-US10262.  
 PR 12-JUN-1996; 96US-0017843.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PI Appelbaum ER, Hu J;  
 XX WPI: 1998-052309/05.  
 DR N-PsDB: AAV02295.  
 DR XX  
 XX DNA encoding human cytokine-peptide hormone receptor - useful for  
 PT treating preventing or diagnosing, e.g. lowered resistance to  
 PT infection, asthma, allergy, or haematopoietic disease  
 XX  
 XX Claim 15; Fig 1; 75pp; English.  
 PS  
 XX The sequence is that of the human cytokine/peptide hormone receptor  
 CC (HR-1 receptor). This, or it's activators or agonists, can be used to  
 CC treat, prevent or diagnose predisposition to lowered resistance to  
 CC infection, asthma, allergic or haematopoietic disorders, e.g. where  
 CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,  
 CC neutropenia or cytotoxic treatments for cancer. Antagonists of the  
 CC receptor, e.g. antibodies or fragments of it may be used to treat  
 CC conditions associated with overexpression of the HR-1 receptor, e.g.  
 CC those listed above. Antibodies may also be used to assay levels of HR-1  
 CC receptor, overexpression of which may be diagnostic of tumours, by usual  
 CC immunoassays; to isolate and identify HR-1 receptor-expressing cells; or  
 CC for affinity purification of the HR-1 receptor.  
 XX  
 XX Sequence 380 AA;  
 SQ

Query Match 100.0%; Score 2104; DB 19; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 2e-197;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAFVCLAIGCLYTLFISTFCTSSSDPEIKVNPQDEIVDPGLGYLQWQPPSLD 60  
 Db 1 MAFVCLAIGCLYTLFISTFCTSSSDPEIKVNPQDEIVDPGLGYLQWQPPSLD 60  
 QY 61 HFKECTVEYELKRNIGSETWKTITTKNLHKDGLDKKGIKAKIHTLLPQCCTNGSEVQ 120  
 Db 61 HFKECTVEYELKRNIGSETWKTITTKNLHKDGLDKKGIKAKIHTLLPQCCTNGSEVQ 120  
 QY 121 SSMAETTYWISPOGIPETKVDMDCVYNNWOYLCSMRPGIGVLLDTYNLFWEGLDH 180  
 Db 121 SSMAETTYWISPOGIPETKVDMDCVYNNWOYLCSMRPGIGVLLDTYNLFWEGLDH 180  
 QY 181 ALOCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTPOLQNTVRLP 240  
 Db 181 ALOCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTPOLQNTVRLP 240  
 QY 241 PVLFTFRESSCEIKLKWISIPGPIPARCFDEIEIRDDDTTLVATVAVENETYLKTTNE 300  
 Db 241 PVLFTFRESSCEIKLKWISIPGPIPARCFDEIEIRDDDTTLVATVAVENETYLKTTNE 300  
 QY 301 TROLCEVVRKVNITYCSDGIMSEMSDKQCEGEDLSKRTLLRFLPRGFTLLIVIFVTG 360  
 Db 301 TROLCEVVRKVNITYCSDGIMSEMSDKQCEGEDLSKRTLLRFLPRGFTLLIVIFVTG 360  
 QY 361 LLKRPNTPYRKMIPEFCDT 380  
 Db 361 LLKRPNTPYRKMIPEFCDT 380  
 RESULT 7  
 ID AAY95296  
 XX AAY95296 standard; Protein: 380 AA.  
 AC AAY95296:  
 XX 12-SEP-2000 (first entry)  
 DT XX  
 XX IL-13 binding chain of human IL-13 receptor.  
 DE XX  
 XX Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;  
 KW cytokine receptor; haematopoietic receptor; atopy; allergy; asthma;  
 KW immune complex disease; lupus; nephritis; thyroiditis;  
 KW Grave's disease; inflammatory; infection; therapy; antiasthmatic;  
 KW antiinflammatory; antiasthmatic; vaccine.  
 XX Homo sapiens.  
 OS XX  
 XX Key  
 FH Peptide 1..25 location/Qualifiers  
 FT /note= "signal peptide"  
 FT Protein 26..380  
 FT /note= "mature protein"  
 FT Domain 26..341  
 FT /note= "extracellular domain; a polypeptide  
 FT comprising amino acids 22-334 is  
 FT specifically claimed in Claim 11(e)"  
 FT Domain 342..362  
 FT /note= "transmembrane domain"  
 FT Domain 363..380  
 FT /note= "intracellular domain; a polypeptide  
 FT comprising amino acids 257-383 is  
 FT specifically claimed in Claim 11(f)"  
 PN WO200036103-A1.  
 XX 22-JUN-2000.  
 PD 13-DEC-1999; 99WO-US29493.  
 XX

XX 14-DEC-1998; 980S-0211335.  
XX  
PR (GEM ) GENETICS INST INC.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;  
PI Wills-Karp M;  
XX  
XX WPI: 2000-431587/37.  
DR N-PSDB: AAA27912.  
XX  
PT New polynucleotide encoding an interleukin-13 (IL-13) binding chain of  
an IL-13 receptor for treating IGE-mediated conditions, such as atopy,  
PT asthma, Grave's disease and inflammatory conditions of the lung -  
XX  
XX Claim 11(d): Page 53-54; 60pp: English.

CC The present sequence is that of the interleukin-13 binding chain  
CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated  
CC human testis cDNA clone (see AAA27912). IL-13bc is a member of  
CC the haematopoietin receptor family that acts as a mediator of  
CC IL-13. The invention provides methods for the recombinant  
CC production of IL-13bc polypeptides, including claimed full-length  
CC IL-13bc, its extracellular domain, and its intracellular domain.  
CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,  
CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction  
CC of IL-13 and its receptor) can be used to treat conditions in  
CC which IL-13 is implicated, particularly Ige-mediated conditions and  
CC diseases including atopy, allergy, asthma, immune complex diseases  
CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,  
CC thyroiditis and Grave's disease), lung inflammation,  
CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage  
CC activation, IL-13bc proteins can also be used to enhance macrophage  
CC activation, e.g. in vaccination, treatment of mycobacterial or  
CC intracellular organisms or parasite infections. IL-13bc proteins  
CC may also be used to potentiate the effects of IL-13 in vitro and  
CC in vivo, as diagnostic agents, and to screen for agents capable of  
CC binding to IL-13bc or IL-13 receptor, or which interfere with the  
CC binding of IL-13 to its receptor.

XX  
XX  
SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 21; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MAFVCLAIICLYTLFISTFECTSSDTEIKVNPDPDEIVDPGLYLYQWOPPLSLD 60  
1 MAFVCLAIICLYTLFISTFECTSSDTEIKVNPDPDEIVDPGLYLYQWOPPLSLD 60  
1 HFKECTVEELKYNIGSETWKTITTKNLHKDGFDLKGIKIAKIHLLPQCCTNGSEVQ 120  
61 HFKECTVEELKYNIGSETWKTITTKNLHKDGFDLKGIKIAKIHLLPQCCTNGSEVQ 120  
61 HFKECTVEELKYNIGSETWKTITTKNLHKDGFDLKGIKIAKIHLLPQCCTNGSEVQ 120  
0Y 121 SSMAETTYWISPOGIPETKVODMDCVYYNMQYLLCSMKPGIGVLDITVNLFFWYEGLDH 180  
121 SSMAETTYWISPOGIPETKVODMDCVYYNMQYLLCSMKPGIGVLDITVNLFFWYEGLDH 180  
121 SSMAETTYWISPOGIPETKVODMDCVYYNMQYLLCSMKPGIGVLDITVNLFFWYEGLDH 180  
0Y 181 ALQCVDIYKADGQINIGCFPLEASDYKDFIYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
181 ALQCVDIYKADGQINIGCFPLEASDYKDFIYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
181 ALQCVDIYKADGQINIGCFPLEASDYKDFIYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
0Y 241 PVLTLFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDITVLTAVENETVTLKTTNE 300  
241 PVLTLFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDITVLTAVENETVTLKTTNE 300  
241 PVLTLFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDITVLTAVENETVTLKTTNE 300  
0Y 301 TROLCFVRSKVNIGSDGQIMSEMSKQCEGEGEDLSKKTLLRFMLPFGFILLIVFTVG 360  
301 TROLCFVRSKVNIGSDGQIMSEMSKQCEGEGEDLSKKTLLRFMLPFGFILLIVFTVG 360  
301 TROLCFVRSKVNIGSDGQIMSEMSKQCEGEGEDLSKKTLLRFMLPFGFILLIVFTVG 360  
0Y 361 LLRRKPTNTPKMIPEFCDT 380  
361 LLRRKPTNTPKMIPEFCDT 380

Db 361 LLRRKPTNTPKMIPEFCDT 380

RESULT 8  
AAG63812  
ID AAG63812 standard; Protein; 380 AA.  
XX  
XX AAG63812;  
AC  
XX  
XX 29-OCW-2001 (first entry)  
DT  
XX  
XX Amino acid sequence of human interleukin-13 receptor subunit alpha 2.  
DE  
XX  
XX Human; interleukin-13 receptor subunit alpha 2; IL-13Ra1pha2; cancer;  
KW testis antigen; immune response; glioma cell.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200158479-A1.  
PN  
XX  
XX 16-AUG-2001.  
PD  
XX  
XX 08-FEB-2001; 2001MO-US04384.  
PE  
XX  
XX 08-FEB-2000; 2000US-0181000.  
PR  
XX  
XX (PENN-) PENN STATE RES FOUND.  
PA  
XX  
XX Debinski W;  
PI  
XX  
XX WPI: 2001-522435/57.  
DR N-PSDB: AAH74791.  
DR

PT Stimulating immune response against interleukin-13 receptor alpha2  
PT subunit in a subject having or at risk of developing gliomas, involves  
PT formulating a vaccine comprising an agent that stimulates immune  
PT response against the subunit -  
XX  
XX  
PS Claim 3; Fig 1; 66pp: English.

CC The present sequence represents a human interleukin-13 receptor subunit  
CC alpha 2 (IL-13Ra1pha2), which is a cancer/testis antigen. The  
CC specification describes a method for stimulating immune response  
CC against IL-13Ra1pha2 subunit. The method is used for stimulating  
CC immune response against IL-13Ra1pha2 in a human being having or at  
CC risk of developing a cancer having glioma cells expressing IL-13Ra1pha2.  
CC The polypeptides and polynucleotides are useful for preventing and/or  
CC treating cancers e.g., high grade gliomas (HGG).

XX  
XX  
SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 22; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MAFVCLAIICLYTLFISTFECTSSDTEIKVNPDPDEIVDPGLYLYQWOPPLSLD 60  
1 MAFVCLAIICLYTLFISTFECTSSDTEIKVNPDPDEIVDPGLYLYQWOPPLSLD 60  
1 HFKECTVEELKYNIGSETWKTITTKNLHKDGFDLKGIKIAKIHLLPQCCTNGSEVQ 120  
61 HFKECTVEELKYNIGSETWKTITTKNLHKDGFDLKGIKIAKIHLLPQCCTNGSEVQ 120  
61 HFKECTVEELKYNIGSETWKTITTKNLHKDGFDLKGIKIAKIHLLPQCCTNGSEVQ 120  
0Y 121 SSMAETTYWISPOGIPETKVODMDCVYYNMQYLLCSMKPGIGVLDITVNLFFWYEGLDH 180  
121 SSMAETTYWISPOGIPETKVODMDCVYYNMQYLLCSMKPGIGVLDITVNLFFWYEGLDH 180  
121 SSMAETTYWISPOGIPETKVODMDCVYYNMQYLLCSMKPGIGVLDITVNLFFWYEGLDH 180  
0Y 181 ALQCVDIYKADGQINIGCFPLEASDYKDFIYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
181 ALQCVDIYKADGQINIGCFPLEASDYKDFIYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
181 ALQCVDIYKADGQINIGCFPLEASDYKDFIYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
0Y 241 PVLTLFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDITVLTAVENETVTLKTTNE 300  
241 PVLTLFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDITVLTAVENETVTLKTTNE 300  
241 PVLTLFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDITVLTAVENETVTLKTTNE 300

Db 241 PVLFTFTRESSCEIKLWMSIPGIPARCFDYEIEIREDDTTLVATVENEYTLTKTNE 300  
QY 301 TRQLCFVRSKVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPGFLLIVFTVG 360  
Db 301 TRQLCFVRSKVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPGFLLIVFTVG 360  
QY 361 LLRRKPMTPKMIPEFCDF 380  
Db 361 LLRRKPMTPKMIPEFCDF 380  
RESULT 9  
AAV72136  
ID AAV72136 standard; Protein; 380 AA.  
XX AAV72136;  
AC  
XX 24-APR-2001 (first entry)  
XX Human Interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).  
XX Human: IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;  
KW therapy; tissue fibrosis; Schistosoma infection; surgical incision;  
KW cytoslatic; wound; IL-13 related condition; allergic condition;  
KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;  
KW macrophage activation.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..25  
FT /label= signal\_peptide  
FT 1..81  
FT /note= "this region is identical to the translated  
FT sequence of an expressed sequence tag (EST) identified  
FT as y939f10.r1 human cDNA clone 41648 5"  
FT 26..380  
FT /label= Mature\_human\_interleukin (IL)-13\_binding\_chain\_  
FT of IL-13\_receptor  
FT 26..341  
FT /note= "Extracellular domain; this region is specifically  
FT claimed in claims 1e, 6e, 15e and 23e"  
FT 342..362  
FT /note= "Transmembrane domain"  
FT 363..380  
FT /note= "intracellular domain; this region is specifically  
FT claimed in claims 1f, 6f, 15f and 23f"  
PN WO200078336-A1.  
XX 28-DEC-2000.  
PD 21-JUN-2000; 2000WO-US17103.  
PE 21-JUN-1999; 99US-0334512.  
PR (GEMV ) GENETICS INST INC.  
PA (UYJO ) UNIV JOHN HOPKINS.  
XX Collins M, Donaldson D, Fitz L, Neben T, Whilters MJ, Wood C;  
PI Wills-Karp M;  
XX  
XX WPI: 2001-080753/09.  
DR N-PSDB: AADD2335.  
XX  
XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis  
PT in a mammalian subject, involves administering a pharmaceutical  
PT composition comprising IL-13 antagonist -  
XX  
PS Claim 1a: Page 69-70; 72pp; English.  
XX  
CC The invention relates to a method of treating, or inhibiting  
CC the formation of tissue fibrosis in mammals, which involves

CC administering a pharmaceutical composition comprising interleukin  
CC (IL)-13 antagonist. The protein of the invention is useful for  
CC treating tissue fibrosis resulting from infection with Schistosoma  
CC or from healing of a wound which is a surgical incision, or  
CC inhibiting formation of tissue fibrosis which affects tissues such  
CC as liver, skin epidermis and endoderms, muscle, tendon, cartilage,  
CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,  
CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,  
CC biliary tract and gut. It is also used in the treatment or modulation  
CC of various IL-13 related conditions such as allergic conditions,  
CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.  
CC The present sequence is human interleukin (IL)-13  
CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used  
CC to potentiate the effects of IL-13. This protein is also used to  
CC enhance macrophage activation and hence can be used in vaccination  
CC or treatment of mycobacterial or parasitic infections.  
XX  
XX Sequence 380 AA:  
QY 1 MAFVCLAIGCLYPTLSTFTGCTSSDPEIKVNPDPFEIYDPGLGYLQMPPLSLD 60  
Db 1 MAFVCLAIGCLYPTLSTFTGCTSSDPEIKVNPDPFEIYDPGLGYLQMPPLSLD 60  
QY 61 HFKECTVEYELKRYNIGSEFWKTIITNHLHYKDGFDLNGKIEAKIHTLLPMQCTNGSEVQ 120  
Db 61 HFKECTVEYELKRYNIGSEFWKTIITNHLHYKDGFDLNGKIEAKIHTLLPMQCTNGSEVQ 120  
QY 121 SSWAETTYWISPOGIEPTFKVODMDCVYNNQYLCSMKPGIGVLDPNNYLFYVEGLDH 180  
Db 121 SSWAETTYWISPOGIEPTFKVODMDCVYNNQYLCSMKPGIGVLDPNNYLFYVEGLDH 180  
QY 181 ALQGVYIKADGQNGIGRPFYLEASDYKDFYICVNGSSEKPKRSYFTFQLOQIVAPLP 240  
Db 181 ALQGVYIKADGQNGIGRPFYLEASDYKDFYICVNGSSEKPKRSYFTFQLOQIVAPLP 240  
QY 241 PVLFTFTRESSCEIKLWMSIPGIPARCFDYEIEIREDDTTLVATVENEYTLTKTNE 300  
Db 241 PVLFTFTRESSCEIKLWMSIPGIPARCFDYEIEIREDDTTLVATVENEYTLTKTNE 300  
QY 301 TRQLCFVRSKVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPGFLLIVFTVG 360  
Db 301 TRQLCFVRSKVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPGFLLIVFTVG 360  
QY 361 LLRRKPMTPKMIPEFCDF 380  
Db 361 LLRRKPMTPKMIPEFCDF 380  
RESULT 10  
AAB29748  
ID AAB29748 standard; Protein; 380 AA.  
XX  
XX AAB29748;  
XX  
XX 23-FEB-2001 (first entry)  
DE Human IL-13 receptor IL-13 binding chain (IL-13bc).  
XX  
XX  
KW Human: IL-13 receptor; interleukin-13; IL-13 binding chain;  
KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnereary;  
KW wound healing; schistosoma infection; liver; skin; muscle;  
KW cartilage; cardiac tissue; lung tissue; uterine tissue;  
KW intestinal tissue; vascular tissue; neural tissue.  
XX  
OS Homo sapiens.  
XX  
XX WO200064944-A1.  
PN 02-NOV-2000.  
XX

XX 28-APR-2000; 2000MO-US11612.  
PF  
XX  
XX 28-APR-1999; 99US-0301808.  
PR  
XX  
PA (GEMV ) GENETICS INST INC.  
PI Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Filtz L, Neben T;  
PI Whilters MJ, Wood C;  
DR WPI: 2001-024676/03.  
DR N-PSDB; AAC81416.  
PT Treating or inhibiting tissue fibrosis resulting from infection with  
PT schistosoma and wound healing involves administering interleukin-13 or  
PT interleukin-4 antagonist  
XX  
PS Claim 1; Page 76-77; 82pp; English.  
XX  
XX The invention relates to a method of treating fibrosis in a mammal  
CC by administering an interleukin-13 (IL-13) antagonist or an IL-4  
CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding  
CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or  
CC soluble fragments thereof. The method is useful for treating or  
CC inhibiting the formation of tissue fibrosis resulting from the healing  
CC of a wound, including a surgical incision wound, or from infection with  
CC schistosoma. The method may be used to treat fibrosis in a variety of  
CC tissues, particularly liver tissue, but also skin epidermis, skin  
CC endoderms, muscle, tendon, cartilage, cardiac tissue, pancreatic  
CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,  
CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut  
CC tissue. The present sequence represents human IL-13bc.  
XX  
XX  
SQ Sequence 380 AA:  
Y  
Query Match 100.0%; Score 2104; DB 22; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 MATVCLAIIGLYFLSTFGCTSSDTEIKVNPPODFEIVDPGYGLYLQWQPLSLD 60  
1 MAEVCLAIIGLYFLSTFGCTSSDTEIKVNPPODFEIVDPGYGLYLQWQPLSLD 60  
DB 1 MAEVCLAIIGLYFLSTFGCTSSDTEIKVNPPODFEIVDPGYGLYLQWQPLSLD 60  
Y 61 HFKECTVEYELKYNIGSETMKTITITKNLHYKDGFDLNGIEAKIHTLPMQCTNGSEVQ 120  
61 HFKECTVEYELKYNIGSETMKTITITKNLHYKDGFDLNGIEAKIHTLPMQCTNGSEVQ 120  
DB 61 HFKECTVEYELKYNIGSETMKTITITKNLHYKDGFDLNGIEAKIHTLPMQCTNGSEVQ 120  
Y 121 SSMAETTYWISPGIPIETKQVDMCVYNNQYLLCSWKPEIGVLDITNVMFLWYEGLDH 180  
121 SSMAETTYWISPGIPIETKQVDMCVYNNQYLLCSWKPEIGVLDITNVMFLWYEGLDH 180  
DB 121 SSMAETTYWISPGIPIETKQVDMCVYNNQYLLCSWKPEIGVLDITNVMFLWYEGLDH 180  
Y 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSEKPKIRSSYFTQLONIYKPLP 240  
181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSEKPKIRSSYFTQLONIYKPLP 240  
DB 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSEKPKIRSSYFTQLONIYKPLP 240  
Y 241 PVLVFTRESSCEIKLKWISPLGPPIPCFDEYIEIRREDDTTLVATVENEYTLTKTNE 300  
241 PVLVFTRESSCEIKLKWISPLGPPIPCFDEYIEIRREDDTTLVATVENEYTLTKTNE 300  
DB 241 PVLVFTRESSCEIKLKWISPLGPPIPCFDEYIEIRREDDTTLVATVENEYTLTKTNE 300  
Y 301 TROLCFVNRKVNIVYCSDDDIWSEMSKOCWEGEDLSKTLRLFWLPGFILLIVFVTG 360  
301 TROLCFVNRKVNIVYCSDDDIWSEMSKOCWEGEDLSKTLRLFWLPGFILLIVFVTG 360  
DB 301 TROLCFVNRKVNIVYCSDDDIWSEMSKOCWEGEDLSKTLRLFWLPGFILLIVFVTG 360  
Y 361 LLLRKPTVYKMIPEFCDF 380  
361 LLLRKPTVYKMIPEFCDF 380  
DB 361 LLLRKPTVYKMIPEFCDF 380

RESULT 11

AAM49201

ID AAM49201 standard; protein; 380 AA.

XX  
AC, AAM49201;

XX 28-JUN-2002 (first entry)  
DT  
XX  
XX Human IL-13R alpha-2 chain, SEQ ID NO:1.  
DE  
XX  
XX Human; IL-13R alpha-2 chain; interleukin-13 receptor; sensitisation;  
KW IL-13 immunocoujugate; immunotoxin; growth inhibition; cancer; tumour;  
KW brain; head and neck; squamous cell carcinoma; breast; liver; lung;  
KW mesothelioma; pancreatic; colon; gastric; ovarian; renal; bladder;  
KW prostate; testicular; skin; cervical; uterine; sarcoma; cytostatic;  
KW gene therapy; drug targeting; receptor.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200217968-A2.  
PN  
XX  
XX 07-MAR-2002.  
PD  
XX  
XX 15-AUG-2001; 2001MO-US25663.  
PF  
XX  
XX 31-AUG-2000; 2000US-229842P.  
PR  
XX  
XX (USSR ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX  
XX Puri RK;  
XX WPI: 2002-329734/36.  
XX N-PSDB; ABL55245.  
DR  
XX  
XX Use of nucleic acid or vector encoding interleukin-13 receptor alpha 2  
PT chain polypeptide that binds IL-13, for sensitizing a cancer cell e.g.  
PT brain cancer cell to effector molecule or inhibiting growth of cancer  
PT cell -  
XX  
PS Claim 1; Page -: 80pp; English.  
XX  
XX The invention relates to the use of a nucleic acid or vector  
CC encoding a polypeptide with at least 70% identity to interleukin-13  
CC receptor alpha-2 chain (IL-13R alpha-2; AAM49201) for rendering a  
CC cancer cell sensitive to IL-13R-targeted immunocoujugates or for  
CC inhibiting the growth of a cancer cell. In some cancers that exhibit  
CC little or no expression of IL-13R, transfection with the IL-13R  
CC alpha-2 chain is sufficient to inhibit growth, while in  
CC other such cancers, the introduction of the IL-13R alpha-2 chain enables  
CC immunocoujugates (such as immunotoxins) that comprise IL-13 to be  
CC targeted to the cancer cells. The method of the invention also results  
CC in the inhibition or death of cells in the tumour which were not  
CC directly transfected with the IL-13R alpha-2 chain. It is thought that  
CC transfection of at least some of the cells of a tumour with the IL-13R  
CC alpha-2 chain causes the secretion of a cytokine or other factor that  
CC attracts neutrophils, macrophages, or other lymphocytes to the tumour,  
CC which are then activated to kill the tumour cells. Because a nucleic acid  
CC encoding just the IL-13R alpha-2 chain is used, rather than a much larger  
CC nucleic acid encoding the multiple chains of the entire IL-13R, the  
CC transfection process is likely to be easier, and there should be a larger  
CC choice of vectors that can be used for transfection. A wide range of  
CC cancers can be treated using the methods of the invention, including  
CC brain cancer, head and neck cancer (preferably squamous cell carcinoma),  
CC breast cancer, liver cancer, lung cancer, mesothelioma, pancreatic  
CC cancer, colon cancer, gastric cancer, ovarian cancer, renal cancer,  
CC bladder cancer, prostate cancer, testicular cancer, skin cancer, cervical  
CC cancer, uterine cancer, or sarcoma. The present sequence represents  
CC the human IL-13R alpha-2 chain which is specifically claimed for  
CC use in the method of the invention.  
CC Note: The present sequence is not shown in the specification, but was  
CC obtained from Genbank using the accession number (X95302) referred to on  
CC page 13.  
XX  
XX  
SQ Sequence 380 AA:  
Y  
Query Match 100.0%; Score 2104; DB 23; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 MAFVCLAIGCLYTFLLISTFECTSSSDTEIKVNPPODEIVDPGYLGVLVQMOPPLSLD 60  
 DB 1 MAFVCLAIGCLYTFLLISTFECTSSSDTEIKVNPPODEIVDPGYLGVLVQMOPPLSLD 60  
 QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLKKGIKIAKIHTLLPMOCTNGSEVQ 120  
 DB 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLKKGIKIAKIHTLLPMOCTNGSEVQ 120  
 QY 121 SSMAETTYWISPOGIPETKVDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGIDH 180  
 DB 121 SSMAETTYWISPOGIPETKVDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGIDH 180  
 QY 181 ALQCVDIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQIVKPLP 240  
 DB 181 ALQCVDIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQIVKPLP 240  
 241 PVYLTFTRESSCEIKLWKSIPLAGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTTNE 300  
 241 PVYLTFTRESSCEIKLWKSIPLAGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTTNE 300  
 QY 301 TROLCFVVRKVNINYCSDGIMSEMSDKQCEGDELKSKTLLRMLPFGFILLIVIPVTG 360  
 DB 301 TROLCFVVRKVNINYCSDGIMSEMSDKQCEGDELKSKTLLRMLPFGFILLIVIPVTG 360  
 QY 361 LLRKPNTPYKMIPEFFCDT 380  
 DB 361 LLRKPNTPYKMIPEFFCDT 380  
 RESULT 12  
 AAM36614  
 ID AAM36614 standard; Protein: 380 AA.  
 AC AAM36614:  
 XX 30-MAR-1998 (first entry)  
 DE Human zcytor2 cytokine receptor protein.  
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 XX Infertility; antagonist; contraceptive; diagnostic; therapeutic.  
 OS Homo sapiens.  
 XX W09733913-A1.  
 18-SEP-1997.  
 PF 12-MAR-1997; 97WO-US04043.  
 PR 13-MAR-1996; 96US-0013345.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Baumgartner JM, Farrah TM, Foster DC, Grant FJ,  
 PI O'Hara PJ;  
 XX WPI; 1997-4/0820/43.  
 DR N-PSDB; AAT96783.  
 XX New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Claim 1; Page 51-53; 79pp; English.  
 XX This sequence represents a novel ligand-binding receptor, zcytor2, which  
 CC shares homology with cytokine receptors and was isolated from a human  
 CC testis cDNA library. The resulting polypeptide is a receptor for  
 CC cytokines (particularly Interleukin-13) and is expressed on the surface  
 CC of testicular cells, probably being involved in spermatogenesis. It can  
 CC be used to detect ligands that promote proliferation and/or

CC differentiation of such cells in cultures and may also be used to treat  
 CC infertility. Antagonists of this receptor may be used to characterise  
 CC ligand-receptor interactions and as male-specific contraceptives. By  
 CC blocking the action of IL-13, receptor antagonists and ligand-binding  
 CC this receptor can also be used to modulate immune function, e.g. in  
 CC allergy and asthma, as a diagnostic to determine circulating levels of  
 CC ligand and also to isolate and purify ligands. Antibodies can be used to  
 CC assay circulating receptor (an abnormal level may be indicative of  
 CC disease such as cancer), for labelling cells that express the receptor,  
 CC and therapeutically as antagonist.  
 XX Sequence 380 AA:  
 SQ  
 Query Match 98.8%; Score 2078; DB 18; Length 380;  
 Best Local Similarity 99.2%; Pred. No. 6.9e-195;  
 Matches 377; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MAFVCLAIGCLYTFLLISTFECTSSSDTEIKVNPPODEIVDPGYLGVLVQMOPPLSLD 60  
 DB 1 MAFVCLAIGCLYTFLLISTFECTSSSDTEIKVNPPODEIVDPGYLGVLVQMOPPLSLD 60  
 QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLKKGIKIAKIHTLLPMOCTNGSEVQ 120  
 DB 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLKKGIKIAKIHTLLPMOCTNGSEVQ 120  
 QY 121 SSMAETTYWISPOGIPETKVDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGIDH 180  
 DB 121 SSMAETTYWISPOGIPETKVDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGIDH 180  
 QY 181 ALQCVDIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQIVKPLP 240  
 DB 181 ALQCVDIKADGONIGCFPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQIVKPLP 240  
 QY 241 PVYLTFTRESSCEIKLWKSIPLAGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTTNE 300  
 DB 241 PVYLTFTRESSCEIKLWKSIPLAGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTTNE 300  
 QY 301 TROLCFVVRKVNINYCSDGIMSEMSDKQCEGDELKSKTLLRMLPFGFILLIVIPVTG 360  
 DB 301 TROLCFVVRKVNINYCSDGIMSEMSDKQCEGDELKSKTLLRMLPFGFILLIVIPVTG 360  
 QY 361 LLRKPNTPYKMIPEFFCDT 380  
 DB 361 LLRKPNTPYKMIPEFFCDT 380  
 RESULT 13  
 AAM36616  
 ID AAM36616 standard; Protein: 372 AA.  
 AC AAM36616:  
 XX 30-MAR-1998 (first entry)  
 DE Celebus macaque zcytor2 protein.  
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 XX Infertility; antagonist; contraceptive; diagnostic; therapeutic.  
 OS Macaque sp.  
 XX Key location/Qualifiers  
 FT Protein 1..372  
 FT /label= zcytor2  
 FT /note= "partial protein sequence"  
 XX W09733913-A1.  
 XX 18-SEP-1997.  
 PD 12-MAR-1997; 97WO-US04043.  
 PF 13-MAR-1996; 96US-0013345.

XX (ZYMO ) ZYMOGENETICS INC.  
PA Baumgartner JW, Farrah TM, Foster DC, Grant FU,  
XX O'Hara PJ.  
PI WPI: 1997-470820/43.  
DR N-PSDB; AAT96784.  
XX  
XX New nucleic acid encoding testis-specific cytokine receptor - useful  
PT for identification of ligands or antagonists, potentially for use as  
PT male contraceptives or for infertility treatment  
XX  
XX Example 4; Page 56-57; 79pp; English.  
XX  
XX This sequence represents a novel ligand-binding receptor, Zcytor2,  
CC which shares homology with cytokine receptors and is isolated from  
CC testis tissue obtained from a Celebus macaque. The resulting polypeptide  
CC is a receptor for cytokines (particularly interleukin-13) and is  
CC expressed on the surface of testicular cells, probably being involved in  
CC spermatogenesis. It can be used to detect ligands promoting proliferation  
CC and/or differentiation of such cells in cultures and may also be used to  
CC treat infertility. Antagonists of this receptor may be used to  
CC characterise ligand-receptor interactions and as male-specific  
CC contraceptives. By blocking the action of IL-13, receptor antagonists and  
CC ligand-binding this receptor can also be used to modulate immune  
CC function, e.g. in allergy and asthma, as a diagnostic to determine  
CC circulating levels of ligand and also to isolate and purify ligands.  
CC Antibodies can be used to assay circulating receptor (an abnormal level  
CC may be indicative of disease such as cancer), for labelling cells that  
CC express the receptor, and therapeutically as antagonist.  
XX  
XX Sequence 372 AA;  
SQ  
Query Match 88.1%; Score 1853; DB 18; Length 372;  
Best Local Similarity 92.2%; Pred. No. 7, 4e-173;  
Matches 34; Conservative 7; Mismatches 22; Indels 0; Gaps 0;  
QY 1 MAFVCLAIGCLYTLTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWOPPLSLD 60  
Db 1 MAFVLAIRCLCTFLISTFTGCTSTDEIKVNPQDFEIVDPGYLYLQWOPPLSLD 60  
QY 61 HFRCCTVEYLKYNIGSETKTITIKLHKDGFDLNKIGIEAKITHLLPMQCTNGSEVQ 120  
Db 61 NFKCTVEYLKYNIGSETKTITIKLHKDGFDLNKIGIEAKITHLLPMQCTNGSEVQ 120  
QY 121 SSMAETTYWISPGIGIPETKVQDMCVYNNQYLLCSWKPFGIGVLDITVNLFWYEGIDH 180  
Db 121 SSMAETATWISPGIGIPETKVQDMCVYNNQYLLCSWKPFGIGVLDITVNLFWYEGIDR 180  
QY 181 ALOCVDYIKADGONICRFPYLEASDKDFITCVNGSSEKPIRSSYFTFOLQNIIVKPLP 240  
Db 181 ALOCVDYIKADGONICRFPYLEASDKDFITCVNGSSEKPIRSSYFTFOLQNIIVKPLP 240  
QY 241 PVYLTFRRESCECEIKLWKSIPLGPIPARCFYEIEIRDDTTLTATVENVETVYLKKTNE 300  
Db 241 PVCLTCTQESLEYELKLMWSIPLGPIPARCFYEIEIRDDTTLTATVENVETVYLKKTNE 300  
QY 301 TROLCFVVRSKVNITCSDDGIMSEMSDKOCWEGEDLSKKTLLRFMLPFGFLLIVIEVTG 360  
Db 301 TROLCFVVRSKVNITCSDDGIMSEMSDKOCWEGEDLSKKTLLRFMLPFGFLLIVIEVTG 360  
QY 361 LLLRKPNTYPRM 372  
Db 361 LLLCRKDSYPRM 372

DT 26-FEB-2002 (first entry)  
XX  
DE Human soluble cytokine IL-13 receptor alpha2 (IL-13RA2) protein.  
XX  
KW Human; zalphal1; cytokine receptor; immunosuppressive; cytostatic;  
KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;  
KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;  
KW viral infection; IL-13 receptor alpha2; IL-13RA2.  
XX  
OS Homo sapiens.  
XX  
XX W0200177171-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 03-APR-2001; 2001WO-US10872.  
XX  
XX 05-APR-2000; 2000US-194731P.  
XX  
XX 28-JUL-2000; 2000US-222121P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;  
XX WPI: 2002-025898/03.  
XX N-PSDB; AAD22980.  
XX  
XX Novel soluble receptor polypeptides and polynucleotides used as  
PT cytokine antagonist for stimulating ligand actively-induced  
PT proliferation of hematopoietic cells and for suppressing immune  
PT response in a mammal  
XX  
XX  
PS Disclosure; Page 240-241; 243pp; English.  
XX  
XX The invention relates to an isolated soluble zalphal cytokine receptor  
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for  
CC inhibiting or antagonising the ligand activity-induced proliferation of  
CC hematopoietic cells and haematopoietic cell progenitors preferably  
CC lymphoid cells which are natural killer cells or cytotoxic T cells.  
CC Zalpha is useful for treating immune and inflammatory disorders, for  
CC reducing proliferation of neoplastic B or T cells, for suppressing an  
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is  
CC useful for treating diseases that require immune regulation including  
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,  
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;  
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,  
CC sepsis, viral infection (dengue virus infection) and cancer. The present  
CC sequence is human soluble cytokine IL-13 receptor alpha2 (IL-13RA2)  
CC protein related to the invention.  
XX  
XX Sequence 317 AA;  
SQ  
Query Match 83.8%; Score 1764; DB 23; Length 317;  
Best Local Similarity 100.0%; Pred. No. 3, 1e-164;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 DTEIKVNPPODFEIVDPGYLYLQWOPPLSLDHFKECTVEYLKYNIGSETKTIT 86  
Db 1 DTEIKVNPPODFEIVDPGYLYLQWOPPLSLDHFKECTVEYLKYNIGSETKTIT 86  
QY 87 KNLHYKDGFDLNLKIGIEAKITHLLPMQCTNGSEVOSSMAETTYWISPGIGIPETKVQDMCV 146  
Db 61 KNLHYKDGFDLNLKIGIEAKITHLLPMQCTNGSEVOSSMAETTYWISPGIGIPETKVQDMCV 120  
QY 147 YNNQYLLCSWKPFGIGVLDITVNLFWYEGIDHALDCVDYIKADGONICRFPYLEASD 206  
Db 121 YNNQYLLCSWKPFGIGVLDITVNLFWYEGIDHALDCVDYIKADGONICRFPYLEASD 180  
QY 207 YKDFYICVNGSSEKPIRSSYFTFOLQNIIVKPLPPVYLTFRRESCECEIKLWKSIPLGPI 266  
Db 181 YKDFYICVNGSSEKPIRSSYFTFOLQNIIVKPLPPVYLTFRRESCECEIKLWKSIPLGPI 240

QY 267 ARCPDYIEIREDDTTLVTATVENETYYLTKTNETRQLCFVVRSKVNIYCSDDGIWSEMS 326  
 Db 241 ARCPDYIEIREDDTTLVTATVENETYYLTKTNETRQLCFVVRSKVNIYCSDDGIWSEMS 300  
 QY 327 DKCWEGEDLSKKTLLR 343  
 Db 301 DKCWEGEDLSKKTLLR 317

RESULT 15  
 AAW56261  
 ID AAW56261 standard; Protein: 315 AA.  
 XX  
 AC AAW56261;  
 XX  
 DT 16-SEP-1998 (first entry)

Mature interleukin-13 binding protein.

KM Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;  
 KM autoimmune disease; antibody; immunotherapy.

OS Homo sapiens.

PN WO9810638-A1.

PD 19-MAR-1998.

PF 10-SEP-1997; 97WO-AU00591.

PR 27-FEB-1997; 97AU-0005374.

PR 10-SEP-1996; 96AU-0002262.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;

XX WPI: 1998-207062/18.

DR N-PSDB; AAV22702.

XX New isolated interleukin-13 binding protein - used to develop  
 PT products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection

XX Disclosure; Page 55-56; 69pp; English.

CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.

XX Sequence 315 AA;

Query Match 83.3%; Score 1753; DB 19; Length 315;

Best Local Similarity 100.0%; Pred. No. 3.7e-163;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPQDFEIVDPGIGYLYLWOPPLSLDHFKECTVEYELKYRNIGSETWTKTITKN 88  
 Db 1 EIKVNPQDFEIVDPGIGYLYLWOPPLSLDHFKECTVEYELKYRNIGSETWTKTITKN 60  
 QY 89 LHKKGDFLKNKGIKAIHTLLPMQCTNGSEVOSSMAETTYWISPGIPEKRVQDMDCVY 148  
 Db 61 LHKKGDFLKNKGIKAIHTLLPMQCTNGSEVOSSMAETTYWISPGIPEKRVQDMDCVY 120  
 QY 149 NMQYLCSMKRGIGVLDITNINLFYWEGLDHALQCVDIKADGQNTGCRPPYLEASDYK 208  
 Db 121 NMQYLCSMKRGIGVLDITNINLFYWEGLDHALQCVDIKADGQNTGCRPPYLEASDYK 180

QY 209 DFYICVNGSSSENKPIRSSYFTFOLQNIYKPLPPVYLFTFTRESSCEIKLWSIPLGPIPAR 268  
 Db 181 DFYICVNGSSSENKPIRSSYFTFOLQNIYKPLPPVYLFTFTRESSCEIKLWSIPLGPIPAR 240  
 QY 269 CFDYIEIREDDTTLVTATVENETYYLTKTNETRQLCFVVRSKVNIYCSDDGIWSEMSDK 328  
 Db 241 CFDYIEIREDDTTLVTATVENETYYLTKTNETRQLCFVVRSKVNIYCSDDGIWSEMSDK 300  
 QY 329 QCWEGEDLSKKTLLR 343  
 Db 301 QCWEGEDLSKKTLLR 315

Search completed: January 24, 2003, 19:35:35  
 Job time : 38 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:33:14 : Search time 35 Seconds  
(without alignments)  
2237.083 Million cell updates/sec

Title: US-09-714-792a-4  
Perfect score: 2104  
Sequence: 1 MAFVCLAIICLYTFLISTF.....LLLRKPNTYPKMIPFECDT 380

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1503	71.4	386	6	Q95LF0
2	1194.5	56.8	383	11	O88786
3	1172.5	55.7	385	11	O8VHK6
4	579	27.5	404	13	O90XP8
5	311.5	14.8	420	4	O14633
6	310.5	14.8	386	4	O14631
7	302.5	14.4	405	6	O95LF1
8	298.5	14.2	415	11	O92OK4
9	297	14.1	427	4	O96BB4
10	296	14.1	426	11	O8VHC2
11	292	13.9	333	4	O15469
12	268	12.7	414	11	O92DB8
13	264.5	12.6	349	6	O97597
14	259	12.3	414	11	O99PS3
15	241.5	11.5	279	4	O9UDY5
16	240.5	11.4	249	4	O8MX09

17	222	10.6	368	6	O8S071	O8S071 sus scrofa
18	212.5	10.1	278	11	O8VHR8	O8VHR8 rattus norv
19	187	8.9	611	13	O91BF6	O91BF6 xenopus lae
20	187	8.9	611	13	O9PT10	O9PT10 xenopus lae
21	185.5	8.8	343	13	O9DE01	O9DE01 oncorhynch
22	178	8.5	896	11	O64146	O64146 rattus norv
23	175.5	8.3	896	11	O802X9	O802X9 mus musculu
24	174.5	8.3	611	13	O9PTM9	O9PTM9 xenopus lae
25	173.5	8.2	881	13	O57519	O57519 xenopus lae
26	170	8.1	890	11	O9Z1A0	O9Z1A0 cavia porce
27	167	7.9	622	6	O9N0J7	O9N0J7 callithrix
28	164	7.8	227	6	O9GLM3	O9GLM3 ursus marit
29	159	7.6	608	11	O99JZ1	O99JZ1 mus musculu
30	156	7.4	625	6	O9XS92	O9XS92 trichosurus
31	155	7.4	626	13	O90MG7	O90MG7 cynops pyrr
32	153.5	7.3	918	13	O9W6U9	O9W6U9 gallus gall
33	153	7.3	217	6	O46386	O46386 mustela vis
34	151	7.2	206	4	O16354	O16354 homo sapien
35	151	7.2	268	4	O8TD78	O8TD78 homo sapien
36	151	7.2	288	4	O96P35	O96P35 homo sapien
37	151	7.2	349	4	O9UHJ5	O9UHJ5 homo sapien
38	151	7.2	376	4	O96P35	O96P35 homo sapien
39	147.5	7.0	538	13	O9DFU0	O9DFU0 sparus aura
40	146.5	7.0	422	4	O9UHH5	O9UHH5 homo sapien
41	145.5	6.9	422	4	O75462	O75462 homo sapien
42	143.5	6.8	435	11	O9JMS8	O9JMS8 mus musculu
43	138	6.6	390	4	O9UEH7	O9UEH7 homo sapien
44	135	6.4	346	13	O93404	O93404 oreochromis
45	131	6.2	861	6	O9BEG2	O9BEG2 bos taurus

#### ALIGNMENTS

RESULT 1	ALIGNMENTS
Q95LF0	PRELIMINARY; PRT; 386 AA.
ID Q95LF0	
AC Q95LF0	
DT 01-DEC-2001 (TREMBLrel. 19, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Interleukin 13 receptor alpha chain 2.	
GN IL13RA2.	
GN	
OS Canis familiaris (Dog).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX NCBI_Taxid=9615;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=21287533; PubMed=11389954;	
RA Tang L.;	
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues.";	
RT	
RL Vet. Immunol. Immunopathol. 79:181-195(2001).	
DR EMBL: AB314533; AAL14887.1; -.	
DR InterPro: IPR002996; CRIA.	
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.	
KW Receptor.	
SO SEQUENCE	
Q95LF0	386 AA; 45110 MW; A16PDEF2DD023ED95 CRC64;

Query Match 71.4%; Score 1503; DB 6; Length 386;  
Best Local Similarity 72.9%; Pred. No. 1.2e-121;  
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

QY	1	MAFVCLAIICLYTFLISTFGCTSSDPTETKVNPPQPEIVDPKYLGLYLQMPPLSLD	60
DB	1	MAFLHNDVGFLLYTLVTAFC-SMLSNAEIKVNPPQPEIVDPKYLGLYLQMPPLPPD	59
QY	61	HFKECTVEYELKRYNIGSETWTKTITTKNLHYKDGFDLNGKIEAKIHTLLPMOCNGSEVQ	120
DB	60	NFKECTIEYELKRYNIDSEMKTKITITTKNLHYKDGFDLNGKIEAKIHTLLPMOCNGSEVR	119

Qy	121	SSMETHYWSIPGQIPEKKNODMCCVYNNQYLLCSMKPGIGVLDLNTNVLFTWYBSGDH	180
Db	120	SSMETHYWSIPGQIREKKTIDDMCCVYNNQYLLCSMKPGGAGHFDNLYOLFWEGLDH	179
Qy	181	ALOCEDYIKADGONIGCRFFPLEASDYPKDFICVNGSSSEKPIRSYFYFQLONIYKPLP	240
Db	180	SAECTDYIKVNGKNNGCRRPLESSDYPKDFICVNGSSSEQPIRPSYFYFQLONIYKPM	239
Qy	241	PVYLTFPHESSCEIKLKMSTPLGPIPARCEPYEIEIEDDTLLVTAIVENETTKLTNE	300
Db	240	PDYSLTVKNSSEELNKMNMKRGPIPKPCFYELEFTEEDTQVTTWTTTVEHDIOTRISNE	299
Qy	301	TROICFVVRSKRVNIYCSDDGIWSSMSRQOCWEGEDLSKTLILRFWLPFGFILLVLIVFTG	360
Db	300	SQKICFLVRSAVNIIYCSDDGIWSSMSRQOCWK-G-DINKETLVFPLIPFARVSLFVLVITC	358
Qy	361	LLLRKPNTYKPMI 373	
Db	359	LLLYQRALLKTI 371	

RECORD ID	PRELIMINARY	PRT	383 AA.
088786			
ID 088786	PRELIMINARY	PRT	383 AA.
AC 088786			
DT 01-NOV-1998 (TIREMBLrel. 08, Created)			
DT 01-NOV-1998 (TIREMBLrel. 08, Last sequence update)			
DT 01-MAR-2002 (TIREMBLrel. 20, Last annotation update)			
DE IL-13 receptor alpha 2 (interleukin 13 receptor, alpha 2).			
GN IL13RA2.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=C3H/HEJ; TISSUE=THYMUS;			
RX MEDLINE=98391042; PubMed=9725226;			
RA Donaldson D.D., Whitters M.D., Filtz L., Neben T.Y., Finnerly H.,			
RA Henderson S.L., O'Hara R.M. Jr., Belter D.R., Turner K.J., Wood C.R.,			
RA Collins M.;			
RT "The murine IL-13 receptor alpha 2: molecular cloning,			
RT characterization, and comparison with murine IL-13 receptor alpha 1,"			
RL J. Immunol. 161:2317-2324 (1998).			

RA Strausberg R.;  
 RI Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RI EMBL; U65747; AAC3340.1; -  
 DR EMBL; BC003723; AAH03723.1; -  
 DR HSSP; P16471; 1BP3.  
 DR MGI; MGI:1277954; 1113ra2.  
 DR InterPro; IPR002996; CR1A.  
 DR InterPro; IPR003532; Hemtloopen\_S\_F2.  
 DR PROSITE; PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN\_1.  
 KW Receptor.  
 SO SEQUENCE. 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match	56.8%	Score 1194.5	DB 11	Length 383
Best Local Similarity	58.9%	Pred. No. 5.3e-95		
Matches	219	Conservative	55	Mismatches 91
			Indels	7
			Gaps	3

  

OY	1	MAFVCLAGLCYLFLLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLWQPLSLD	60
	---	-----	----
Db	1	MAFV--HIRCLFLLICTTTGYS---LEIKVNPQDFEILDPGLGLGYLWQMPVVE	54
OY	61	HPKECTVEYELKRYNIGSETWTKTITITKNLHYDGDINKIGAKITHTLLPQCTGSEVO	120
Db	55	KFKGCTLEYELKRYNVDSDSKTITITRNLITYKDGDLNKGIDGKIRTHLISEHCTGSEVO	114
OY	121	SSMAETTYWISFQGIPETRKQVMDQCVVYNNWQYLCSWKGIGIVLLDTNTNLPVWEGLDH	180

Dd	115	SPWIEASVIGIDEGSLEIKIDOMKCIYNNQYLVCMSKPKGTIVYSDNINIMFVYBELDH	174
QY	181	ALOCVDYIKADGONIGCFPLEASDYKDFEYICVNGSSENKPIRSSYFTOLONIVAPLP	240
Dd	175	ALOCADYIQOHKEKWNVCXLSMDSDYKDFEYICVNGSSKLEPISSSYVTEOLONIVAPLP	234
QY	241	PVYLTFTHRESSCEIKIKMSIPLGPIPARCPYELEIEHEDDTLTVAIVAEHETTLKTTNE	300
Dd	235	PEFLTIVSENSIDIRMKMSGTGCPPIPRCXYEYELVIREDDISWESATDKNDKMKIRANE	294
QY	301	TROLCEVVRKVNIVICSDDGIMSEMSDKQOCNEGEDLSKTLTLREWLPFGFLLILVIVPTG	360
Dd	295	SEDLCFEVRCXKVNIVICADGDGIMSEMSBECWEGYTGDPDKITL-ETVAVCLFEFIFILLLC	353
QY	361	LLLRKPNTYPPKM	372
Dd	354	LIVEKEDEPPTL	365

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RESULT 3
Q8VHK6
ID Q8VHK6. PRELIMINARY; PRT; 385 AA.
AC Q8VHK6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Interleukin 13 receptor alpha chain 2.
GN IL13RA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Wu A.; Low W.C.;
RT "Molecular cloning of rat interleukin 13 receptor alpha 2 gene and its
RT expression in rat tissues.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF148818; AAL57513.1; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR005353; Hemicoptn_S_F2.
DR PROSITE: PS01356; HEMATOPO_F0C_S_F2; UNKNOMN.1.
KW RECEPTOR.
SO SEQUENCE 385 AA; 44622 MW; E06F0E434737E2 CRC64;

```

[illegible]



DR InterPro: IPR003532; Hemtopopn\_S\_F2.  
 DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN\_1.  
 KM Receptor; Signal.

FT SIGNAL	1	20
FT CHAIN	21	396

SQ SEQUENCE 396 AA; 44998 MW; 1AB60619842ACDA5 CRC64;

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Query Match Best Local Similarity 14.8%; Score 310.5; DB 4; Length 396;  
 Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

```

OY      27 DTEIKVNPPEFEIVDPGYGLYLQMQPPLSLDFHFKECTVEVELKRNIGSETWTKITTT 86
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       25 DEKISLLEPVNFTIKAVTG-LAQVLLOWKRPNDQEQ-RANNLEYGVKINPKREDYEETRTT 82
OY      87 KNLHYKGDFDLNKGIKAIIHTLLPMOCINGSEFVGSSMAETTYWISPQGIPTKVODMDCV 146
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       83 ES--KCVTIILHKGFSAVSRTLIO---NDHSILLASSMASAEHL-APGSGTSIVALTCT 135
OY      147 -----YYNQXYL-CSKKPGIAGVLDIPNYMLFY-----WGEGDHALQCVDYIRKD 191
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
C        136 TINTEDNYSRLRSKYOVSLHCWTWLGTADAPEDIDYQLLYRYGSMT-----BCOEYSKQT 189
OY      192 -GNIGCFRFP--YLEASDYKDIFYCVNSSESSEKPFRSSSYFFROLNIYPFLPPVLTFTLR 248
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       190 LGRNRACHPFPFTFILSKGRDMALAYLVNSSKSARLPDPQLAFALAIDQINPLVNTAETI 249
OY      249 ESSCEIKLKWSIPLGPICPARCFDEVEIEIREDDFTTLVTAIVENETYLTKTNETROLCFVV 308
           |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       250 EGT-RLSIOMEKPYVASPFICHDEFYEVKIHTRNGYLQLEKLTMNFATISIIDDLSKYDVY 308
OY      309 RSKVNVIYSDDGINSWMESDKCMBEEDLSKTLLEFWLPIFGITLLL-----VFITYGLL 362
           |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       309 RAAYSSMKEREGLNSEWS-QPIYGVNDEHKP--LRDW----FVIIVMATPCIFILLLSLI 361
OY      363 LRKPPTYEKMP 374
Db       362 CKICHIMWKLFEP 373

RESULT 7
ID ID 095LF1 PRELIMITARY: PRI: 405 AA.
AC 095LF1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
De Interleukin 13 receptor alpha chain 1 (Fragment).
GN IL13RA1.
Cc Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21287533; PubMed=11389954;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
RT alpha2) cDNAs and detection of corresponding mRNAs in canine
RT tissues";
RL Vet. Immunopathol. 79:181-195(2001).
DR EMBL; AF314352; AAL14886.1; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003532; Hemtopopn_S_F2.
DR SMART: SM00060; FN3; 1
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KM Receptor.
KW NON_TRAN
SQ SEQUENCE 405 AA; 46328 MW; 926EIACT7BEE5E3FA2 CRC64;
  
```

Query Match 14.4%; Score 302.5; DB 6; Length 405;  
 %Best Local Similarity 27.2%; Pred. No. 5.7e-18;

Matches	100: Conservative	57: Mismatches	142: Indels	69: Gaps	19:
QY	53 WOPPLSLDHFKECTIVEYELKRN-----IGSTMTKTIITKNIHYKDGFDLNGKIEAKIHT	107			
Db	30 WNPPEGAS--PNCOTLRYSFHFNDKODKKIAPET-----HRSKEVPLNERICLOQWS	78			
QY	108 LLPWOC-TNGSVOSSMAETTWIISPOGIPERKVOYDMOCVYVNMQYLLOCSMKPGIGVLLD	166			
Db	79 ----OCSTNESNPISILVEKC-TPPEGGPESAVTELQCVHNIISYKCTWLPGRNTSPD	133			
QY	167 TNYNLFYEGEDHAIQCVDIKADGONIGKFRPY--LEASDYKDFYICVNGSSSENKPR	224			
Db	134 TNYLYLYYHMSLSGKILQCED-IYREGQHIGCFALNLKDSSEFQHSQYIMWKDANKIR	192			
QY	225 SSYFFFOQLONYKPLRP-VYLTFTRESSCEIKLAKSIPGLPIPARCFDEIETREDDTT-	282			
Db	193 PSFNIVPLTSHVKPPPHIKRLEFONGN-LYVQWKNPQN-FYSCLSYQVENVNSQTEP	249			
QY	283 ----LVNATVNEENIYTLKTNETHQLCFVY-----RSKNIYC-SPDGIMS	323			
Db	250 NDIFVEEKKCNSEF---EGNLEBCTICHPVGVLPDLNLYRIVRIYTKKLYEDDKLMS	306			
QY	334 EMSDKQCEGEDLSKRTLLREWLFP-----GFILLVIFYVGL-LLRKPTYP-K	371			
Db	307 NMS-----QAMSIGENTDPTETIYIMLATQYIVAAIITLLLYLRKLIIFPPIPDPGX	361			
QY	372 MIPFFCD 379				
Db	362 IFKEMFGD 369				
RESULT 8					
ID	Q92OK4	PRELIMINARY;	PRT;	415 AA.	
AC	Q92OK4;				
DT	01-MAY-1999 (TREMBLrel. 10, Created)				
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Interleukin-5 receptor alpha precursor.				
GN	GPIL-5A.				
OS	Cavia porcellus (Guinea pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Hystricognath; Caviidae; Cavia.				
OX	NCBI_TaxID=10141;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Norris T.E.;				
RT	"Cloning and Characterization of the Guinea Pig Interleukin-5 receptor				
RL	alpha cDNA."				
RL	Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.				
DR	EMBL: U55215; AAD09361.1; -.				
DR	InterPro: IPR002996; CRA.				
DR	InterPro: IPR003532; Hemtopoptn_S_F2.				
DR	PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWNW_1.				
KW	Receptor; Signal.				
FT	SIGNAL 1 17	POTENTIAL.			
FT	CHAIN 18 415	INTERLEUKIN-5 RECEPTOR ALPHA.			
SO	SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31C04 CRC64;				
Query Match 14.2%; Score 298.5; DB 11; Length 415;					
Best Local Similarity 26.5%; Pred. No. 1.3e-17;					
Matches 103; Conservative 67; Mismatches 172; Indels 47; Gaps 19;					
QY	6 LAIGCLYFLLISTTFGCTSSDTEIKVNPDDFEIVDPGLGYLYLOWQPLSLDHFREC	65			
Db	7 ILIGAIEFLQIDTL-----PDKRFLPLPINFITIKVIG-LAOVVLCHEPMPNCGO-KNV	58			
QY	66 TVEYELKRNIGSGEWKTIITKNIHYKCGFDLNGKIEAKIHTLLPMQCTNSSEVOSSAE	125			
Db	59 NLNHHVKINTPOEEDYE--TRNFOSKCEITLLHQGSASVETIL-WH--GHSLLASSWVS	112			
QY	126 TTYWISPGGIPETVKQDMDCV-----YYNMQ-----YLLCSMKRGIGVLLDTNYNLFY-	173			



Db 113 AEH-KAPGSPGTSIVNLCTTNTAASNYNLKSEVSLHCTHLAGDADBDTQFLYYR 171  
Qy 174 ---WEGLDHALQCVYIKAD-GONIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSY 227  
Db 172 YGPRTE-----ECQESKDLNSNTACWPPRTFIHSKARDRLAVHNGSSNHTATIPFD 225  
Qy 228 FTEQLQNIKVPPLPVYLTFTRESSCEIKLWMSIPLGPIPARCFDEYIEI-REDPTTLYTA 286  
Db 226 QLFDTQALIDQPNPMDVTAETEGS-RLSIQMQKPVSAFPIHCFEYEVKICITKPIYQVEK 284  
Qy 287 TVENETTLTKTINTETROLCTFVVRKVNITYCSDDGIMSEMSDKOCWEEDLSKTKLLR-FW 345  
Db 285 TTTNA--FVSTFDGVSXYSIOVRAAVSPHCRAMGLMSKWS-QPYVVGKE--KKPIAGWFL 339  
Qy 346 LPFGFILLIVFVGLLRKPNTPKMP 374  
Db 340 ITLTAVLCFFILLIFFLICRIYHMTKMP 368

Query Match 14.1%; Score 297; DB 4; Length 427;  
Best Local Similarity 26.3%; Pred. No. 1.8e-17;  
Matches 110; Conservative 63; Mismatches 172; Indels 74; Gaps 21;

Qy 5 CLAIGC-LYTFILSTFGCTSSDTEIKVNPPODFEIVDPGYLYLQWOPPLSLDHF 63  
Db 3 CPALCGLMALILCAGGGGGGAAPETPTVNLVSVENTCTVWTMPPGAS--S 60  
Qy 64 ECTVEY-----ELKYNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHTLLPMOC-TNGS 117  
Db 61 NCSLWYFSHRGDKODKKIAPETRSI-----EVLNMRICLOQVS---QCSINES 107  
Qy 118 EVOSSAEETIYWIS-POGIPETKYQMDVCYVYNNQYILCSKPGICVLLDTNLYLFWYE 176  
Db 108 EKPSILVEKC--ISPPGDEPSAVTELOQCIWHNLSTYMKCSMLPCRNTSPDTNPTLYYVHR 165  
Qy 177 GLDHALQCVYIKADGONIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYTFOLQ 234  
Db 166 SLEKIHQC-ENIFREGQYFGCSFPLTKVXDSSEFQHSYQIWKVNAKIKKISFINIVPLTS 224  
Qy 235 IVKPLPP-VYLTFTRESSCEIKLWMSIPLGPIPARCFDEYIEIREDPT-----LVT 286

Db 225 RVKPDPPHIKNLSEHND---DLVQWENPQNF1-SRCLFEVEEYVNSQTEHNVFYQEA 280  
Qy 287 TVENETTLTKTINTETROLCTFV-----SKVNICY-SDGIMSEMSDKOCWE 332  
Db 281 KCENPEERVENWTS---CEWVPGVLPDPTLNTVIRIKTKNLCEDEDKLMSNSQEM--- 334  
Qy 333 GEDLSKTKLLRFLPF-----GFILLIVFVGL--LKRPNTP-P-KMIPFECF 379  
Db 335 --SIGKRNSTLYITMILLIYVIVAGAIYVLLYLKRLKIIIPPIPDPOKIKREMGD 391

Query Match 14.1%; Score 296; DB 11; Length 426;  
Best Local Similarity 26.1%; Pred. No. 2.2e-17;  
Matches 97; Conservative 56; Mismatches 141; Indels 78; Gaps 17;

Qy 31 KVNPPPODFEIVDPGYLYLQWOPPLSLDHFKECTVEY-----ELKYNIGSETWKTII 85  
Db 28 EVQPPVNTLSVSVENLCTIWTWSPRPGAS--PNCSLRYFSHPDQDKKIAPETRR--- 82  
Qy 86 TKNLHYKDGFDLNGKIEAKIHTLLPMOC-TNGSEVOSMAETIYVISP--OGIPETKYQD 142  
Db 83 -----KKEIPLNKEICLOQVS---QCSINSEKPSPLVKKC--ISPPRRG-SESAVTE 129  
Qy 143 MDCVYVNNQYILCSKPGICVLLDTNNTLFWYEGLDHALQCVYIKADQONIGCRFPYL 202  
Db 130 LQCTWHNLSTYKCSWMLPGKNTSPDTNPTLYVWSSLSKSLQOC-ENIHREQIHGCSFKLT 188  
Qy 203 EA-SDYKDFYICVNGSSENKPIRSSYTFOLQNIKVPPLP-VYLTFTRESSCEIKLWMSI 260  
Db 189 KVESNYEHHNIQIWKVNAKIKRSTYKIVSTSVNKKGPPIKILFLKNGA--LFVQMK 246  
Qy 261 PLGPIPARCFDEYIEIREDPT-----LVTAVENE 291  
Db 247 PON-FSSRCLSYEVEAVNSTQDSYNSLSLEVEEDKCONSEFDRMMEGASCFISGLVANT 305  
Qy 292 TYTLTKTINETROLCTFVVRKVNITYCSDDGIMSEMSDKOCWEEDLSKTKLLRFLPFGFI 351  
Db 306 VYIVRVKTKNLCE-----DNDLMSNWS-----EALSIGKEPSTFTYT--ML 348  
Qy 352 LILVIFVYTGILL 363  
Db 349 LILPVFAVYII 360

RESULT 11  
Q15469 PRELIMINARY; PRT; 333 AA.  
ID Q15469

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AC Q15469;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Soluble Interleukin-5 receptor precursor.
GN HSIL5R4.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
MEDLINE=92121815; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tomiwa A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
RT receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL: X62156; CA44081.1; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003532; Hemtopoptn_S_F2.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 13.9%; Score 292; DB 4; Length 333;
Best Local Similarity 28.0%; Pred. No. 3.6e-17;
Matches 88; Conservative 56; Mismatches 144; Indels 26; Gaps 11;

QY 27 DTEIKVNPDPDEFIVDPGYLYLQMPRLSDHFEKCTVEYELKYRNIGSETWKTIIT 86
DB 25 DEKISLPVPNFTIKYVG-LAQVLLQKPNPDQO--RNVLLEYQVKINAKREDDEYERIT 82
QY 87 KNLHYKGFPLNKGIEKINHTLPLMOCNTNGSEVOSSMAETTYWISPGIGETKYQDMDCV 146
DB 83 ES---KCVTLHKGFSASVFTILO--NDHSLASSWASAEHL-APGSGTSTVNLCT 135
QY 147 -----YNNQYLL-CSMKPGIGVLLDTNYNLFYWEGLDHALQCVDIKAD-GQN 194
DB 136 TMTEDNYSRLRSQVSLHCTWLVGTAPREDTQYFLYRRGSWTE--ECOEYSKDTIGRN 193
QY 195 IGCRRP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLOINIKPLPYVYLFTRESSC 252
DB 194 IACWFPRTFLSKGRDMLAVLVNGSSKHSARPEDDQLFALHAIDQINPPLVTAIEIGT- 252
QY 253 EILKMSIPLGPIPARCFDYEIEIRREDDTLVATVNEETTLKTNETQOLCFVARSKY 312
DB 253 RLSTIQWKPVSAPFPHCFDYEIVKIHNTNGYLOIEKIMTNAFISIIDLSKYDVQVRAAV 312
QY 313 NIYCSDDGINSWMS 326
DB 313 SSMCRAGLMSWMS 326

RESULT 12
Q920B8 PRELIMINARY; PRT; 414 AA.
AC Q920B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin-5 receptor alpha.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F344;
RA Pierrot C., Begue A., Szpirer C., Capron A., Capron M., Khalife J.;
RT "Molecular cloning and characterization of rat IL-5 gene."

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RT chromosomal mapping, analysis of the 5'-upstream region and expression
RT by B cells.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324153; AAK97344.1; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003532; Hemtopoptn_S_F2.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
SQ SEQUENCE 414 AA; 47075 MW; 4340F42F47297D84 CRC64;

Query Match 12.7%; Score 268; DB 11; Length 414;
Best Local Similarity 26.0%; Pred. No. 5.5e-15;
Matches 103; Conservative 64; Mismatches 151; Indels 78; Gaps 20;

QY 17 STEFGCTSSDTEIKVNPDPDEFIVDPGYLYLQMP-----PLSDHFEKCTVEYEL 71
DB 12 SATLHADLSPKFKLLPVPNFTIKATG-LAQVPLHNDPDPDQVPLKHYVKNPQED 70
QY 72 KYRNIGSETWKTIITKNLHYKDFDLNKGIEAKIHPLLMOCNTNGSEVOSSMAETTYWIS 131
DB 71 EYD-----TKNTESKCVTLPHGFAASVFTILK---SIHSPLASWVASAEH-KA 115
QY 132 PGIGETKYQDMDCV-----YNNQY-LLCSMKPGIGVLLDTNYNLFY----WYE 176
DB 116 PGSSGTSVNNLCTTNTVKSHTHFRPYQVSLRCTWLVKDAPEDTQYFLYRFSWTE 175
QY 177 GLDHALQCVYIK-ADGONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQ 233
DB 176 -----ECOEYSKDALNRNACNFPRTFINSKGFQDLAVINSSKHAATKPLDQFTLY 229
QY 234 NIVKPLPYVYLFTRESSCEIKLWSIPLGPIPARCFDYEIEIRDDT-----TLVT-- 285
DB 230 AIDQVNPVNVVTEIERN-SLYIQWKGKPLSAPVHCEKFKLYKNRNGYSQEMNLVTNK 288
QY 286 -ATVEN-EYTIKTNETQOLCFVARSKNYIYCSDDGINSWMSDQWCEGDELSSKTL 342
DB 289 FISKIDVSTYSIQ-----VRAAVSSPCRRMSGSGWMS-PTIYVK---KKPL 333
QY 343 RFW----LPEGFILIVIEVTGLLRKPNTPYKMP 374
DB 334 VEHHLIVLPALICFILLIF--SLICRYHLMTRLP 367

RESULT 13
Q97597 PRELIMINARY; PRT; 349 AA.
AC Q97597;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20080132; PubMed=10614495;
RA Trigona W.L., Brown W.C., Estes D.M.;
RT "Functional implications for signaling via the IL4R/IL13R complex on
RT bovine cells.";
RL Vet. Immunol. Immunopathol. 72:73-79(1999).
DR EMBL: AF074402; AAC98147.1; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003532; Hemtopoptn_S_F2.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 12.6%; Score 264.5; DB 6; Length 349;

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OM protein - protein search, using SW model

Run on: January 24, 2003, 19:34:59 ; Search time 21 Seconds  
(without alignments)  
1739.575 Million cell updates/sec

Title: US-09-714-792a-4

Perfect score: 2104

Sequence: 1 MAFVCIAGICLYTFLISTTF.....LLRRKNTYPKMIPFECDT 380

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Database: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	311.5	14.8	420	2	J21052
2	296	14.1	426	2	SC7773
3	292	13.9	335	2	A40267
4	263	12.5	831	2	U01655
5	247	11.7	415	2	S12357
6	230	10.5	369	2	A42565
7	216.5	10.3	830	2	I50455
8	212.5	10.1	369	2	I49280
9	208	9.9	373	2	A55718
10	195	9.3	878	1	A40091
11	180.5	8.6	897	1	A39255
12	178	8.5	896	2	I56563
13	173.5	8.2	896	1	A35782
14	165	7.8	310	2	A29884
15	165	7.8	412	2	A41070
16	165	7.8	581	2	I45971
17	165	7.8	610	2	A34631
18	165	7.8	610	2	A36116
19	160.5	7.6	303	2	I77524
20	159	7.6	292	2	I77525
21	159	7.6	608	2	I53269
22	151	7.2	288	2	B59405
23	151	7.2	376	2	A59405
24	151	7.2	622	2	A40144
25	150.5	7.2	917	2	I49699
26	149	7.1	616	2	A30304
27	142.5	6.8	400	2	S06945
28	138	6.6	378	2	A40266
29	134.5	6.4	1097	2	S17308

30	133.5	6.3	333	2	S13684	granulocyte-macrop
31	133.5	6.3	378	2	S50040	granulocyte-macrop
32	131.5	6.2	630	2	I51086	prolactin receptor
33	129	6.1	150	2	B34631	lactogen receptor
34	126.5	6.0	918	2	A36337	membrane glycoprot
35	122.5	5.8	286	2	S50039	granulocyte-macrop
36	120.5	5.7	771	2	B38259	granulocyte colony
37	120.5	5.7	783	2	JH0329	granulocyte colony
38	120.5	5.7	863	2	C38252	granulocyte colony
39	112.5	5.3	1630	2	C41214	protein-tyrosine-p
40	111.5	5.3	1557	2	D41214	protein-tyrosine-p
41	110	5.2	6805	2	S20901	titin - rabbit (fr
42	109.5	5.2	918	2	A44257	interleukin-6 sign
43	109.5	5.2	26926	1	I38344	titin, cardiac mus
44	107.5	5.1	638	2	A33991	somatotropin recep
45	107.5	5.1	837	2	A34898	granulocyte colony

#### ALIGNMENTS

RESULT 1  
S21052  
Interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored  
C:Species: Homo sapiens (man)  
C:Date: 22-NOV-1993 #sequence-revision 10-NOV-1995 #text change 01-Dec-2000  
C:Accession: S21052; S21050; S21053; A46175; S78106; S78107  
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.  
J. Exp. Med. 175, 341-351, 1992  
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.  
A:Reference number: S21050; MID:92121815; PMID:1732409  
A:Accession: S21052  
A:Molecule type: DNA  
A:Residues: 1-420 <MU>  
A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844  
A:Experimental source: clone lambda h5R.12  
A:Accession: S21050  
A:Molecule type: DNA  
A:Residues: 1-395 'I' <MU2>  
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840  
A:Experimental source: clone lambda h5R.27  
A:Accession: S21053  
A:Molecule type: mRNA  
A:Residues: 1-332 'K' <MU3>  
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466  
A:Experimental source: clone lambda h5R.25  
R:Tavernier, J.; Tuypens, T.; Plateclink, G.; Verhee, A.; Fiers, W.; Devos, R.  
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992  
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum  
A:Reference number: A46175; MID:92357767; PMID:1495999  
A:Accession: A46175  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 333-420 <TAV>  
A:Experimental source: HL-60 cells and eosinophils  
A:Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)  
R:Murata, Y.  
submitted to the EMBL Data Library, July 1991  
A:Reference number: S78106  
A:Accession: S78106  
A:Molecule type: DNA  
A:Residues: 1-128 'I', 130-395 'I' <MUW>  
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840  
R:Murata, Y.  
submitted to the EMBL Data Library, September 1991  
A:Reference number: S78107  
A:Accession: S78107  
A:Molecule type: mRNA  
A:Residues: 1-128 'I', 130-332 'K' <MU4>  
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466  
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>



A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BA02439.1; PID:g222849  
 A:Experimental source: kidney  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:123/Domain: signal sequence #status predicted <SIG>  
 F:24-83/Product: prolactin receptor #status predicted <MAT>  
 F:36-219/Domain: cytokine receptor homology <CRS1>  
 F:29-425/Domain: cytokine receptor homology <CRS2>  
 F:439-462/Domain: transmembrane #status predicted <TM>  
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (asn) (covale

Query Match 12.5%; Score 263; DB 2; Length 831;  
 Best Local Similarity 26.4%; Pred. No. 7,6e-13;

Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

18 TTTCCTSSDTEIVN--PQDFE---LVDPG-----YIGYLWQOPPLSL 59  
 97 TTFNITVATNEIGSSNDPQYDVTSIVOPSPVNLLETGRSANIMYIMAKSPPLA 156  
 60 DHEKCTVEYELKRYNIGSETWKTIIIRKHLKDGFDLNGKIEAKIHTLLPWOCTNGSEV 119  
 157 DASNHLHYELRIKPEPEKEMETI---SVGVQCKINR-LNAGMRYVAVGCTLDPE 212  
 120 QSSWAETTYWISPG-IPETKVQDMDCVYVNMQYLCSMKPGIGVLLDTNLYFYWEGL 178  
 213 WSEMSERHILIPSGQSPREKPTIIKCRSPEKETFTCMWKGDLGHPNTLLYSKEGE 272  
 179 DHALQCDYIKADQONIGCRPILEASDYKDFYICVAGSSNKRIRSSYTFQLONIYKP 238  
 273 EQVECDY-RTAGPN-SCYFDKHTSFMTIYNITVATNEMGSSSPHVDVYIVOP 330  
 239 LPVYLYFTRESSECEIK---LKWS-IPLPPIPARCFDYEIEIR---EDDTLTATAVEN 290  
 331 DPEVNTVLELKKRPILNRPYLVLTSPPLADYRSGMILTLELKLAKDEGEMETITVGO 390  
 291 ET-VTLKTNETQQLCEVVRKVNIVYSD--GIMSEMSDKOCME-GEDLSKTLRFL 346  
 391 OTQYKMSLNNGKKYI-----IQHCKRPHHGSWSESSNNTYQINDPFRVKMI-VMI 443  
 347 PFGPI-LIIVIPYTGILLKRPNTPKMIP 374  
 444 VLGVLSSLICLIMSWTMYLKGMYTFLP 473

## RESULT 5

Species: Mus musculus (house mouse)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
 C:Accession: S12357  
 R:Takaki, S.; Tomlinaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu, K.  
 EMBO J. 9, 4367-4374, 1990  
 A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.  
 A:Reference number: S12357; MUID:91092260; PMID:2265612  
 A:Accession: S12357  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-415 <TAK>  
 A:Cross-references: GB:D90205; NID:g220465; PIDN:BA01231.1; PID:g220466  
 C:Keywords: cytokine receptor; transmembrane protein

Query Match 11.7%; Score 247; DB 2; Length 415;  
 Best Local Similarity 24.6%; Pred. No. 5,8e-12;

Matches 91; Conservative 70; Mismatches 151; Indels 58; Gaps 18;

34 PQDFEIVDGYGLYLWQOPPLSLDHFKECTVEYELKRYNIGSETWKTIIIRKHLK 93  
 29 PNVFTIKANG-LAQVLLHMDPNPDQEQ-RHVDLEYHKINAPQDEDEYDKTKES---KC 83  
 94 GFLDKIEAKIHTLLPWOCTNGSEVOSSWAETTYWISPGIPETKVQDMDCVYVNM 149  
 84 VTPLEHGFASVITILK---SSHITLASSWVSABL-KAPPSGTSVTNLTCTHTVAVSS 139

150 -----MOY-LLCSMKPGIGVLLDTNLYFYWEGLDHALQCDYIK-ADGONIGCRPP- 200  
 140 HTHLRPYQVSLRCTLWLVGKDAPEDTQYFLYRFEGLVE--KQGEYSKALNRNTRACFP 197  
 201 -YLEASDYKDFYICVAGSSNKRPIRSSYTFPQLONIYKPLPVLITFTRESSECEIKLWS 259  
 198 TFINSGFQGLAVHINSSKRAAIKPPDQLFSLAIDQVNPFRVATYEISN-SLYIQWE 256  
 260 IPLCPPIARCFDYEIEIRDD-----TTLVATVAVENETYLKTNETQQLCEV 308  
 257 KPLSAPFDHCFENYELKRYNIGKNGHIOREKLANFISKIDVSTYSIO-----V 305  
 309 RSKVNIYCSDDGIMSEMSDKOCMEGDSKTLRFM---LPPGFLIIVIFVYTGILLR 364  
 306 RAAVSSPCRMFGRNGEMS-QPIYVGEK--KSLVE-NHLIVLPYACFVLLIF--SLICR 359  
 365 KPNTPKMIIP 374  
 360 VCHLMTRLFP 369

## RESULT 6

Species: Homo sapiens (man)  
 C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
 C:Accession: A42565; A46591; I54332  
 R:Takeshita, T.; Asano, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.  
 Science 257, 379-382, 1992  
 A:Title: Cloning of the gamma chain of the human IL-2 receptor.  
 A:Reference number: A42565; MUID:92335883; PMID:1631559  
 A:Accession: A42565  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid; protein  
 A:Residues: 1-369 <TAK>  
 A:Cross-references: GB:L12186; NID:g303611; PIDN:BA01857.1; PID:g219890  
 A:Experimental source: MOL beta lymphoid cells  
 A:Note: sequence extracted from NCBI backbone (NCBI:109167)  
 R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.  
 J. Biol. Chem. 268, 13601-13608, 1993  
 A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.  
 A:Reference number: A46591; MUID:93293887; PMID:8514792  
 A:Accession: A46591  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-369 <RBS>  
 A:Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058  
 R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993  
 A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11  
 A:Reference number: I54332; MUID:94004847; PMID:8401490  
 A:Accession: I54332  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-369 <RBS>  
 A:Cross-references: GB:L19546; NID:g349631; PIDN:AAC37524.1; PID:g349632  
 C:Genetics:  
 A:Gene: GDB:112RG; SCIDX1; IMD4  
 A:Cross-references: GDB:134807; OMIM:308380  
 A:Map position: Xq13.1-Xq13.1  
 A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3  
 A:Note: defects are associated with an X-linked form of severe combined immunodeficiency  
 C:Superfamily: interleukin-2 receptor gamma chain  
 C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.5%; Score 220; DB 2; Length 369;  
 Best Local Similarity 25.5%; Pred. No. 6,9e-10;

Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

97 LNKIEAKIHTLLPWOCTNGSE-VQSSWAETTYWISPGIPETKVQDMDCVYVNM 155  
 19 LGVGLNTIILT-----PNGNEDTFADEFLTITPTDSLAVSTLPLPVGQCFVFNVEYVNC 72

```

Oy      156 SW-----KPGGIVLLDTNVNLEFYWEGLDH--ALDCVDPIKADGONIGRPFYLEASDY 207
          |         |         |         |         |         |         |         |         |         |
Db      73 TNNSSSEPQ-----TNLTLYHWYKKNSDNDXVQCSHILFSEELITSGQLDKKEHLHY 125
          |         |         |         |         |         |         |         |         |         |
Oy      208 KRFYICLVNGSSSENKPRRSYFTFDLONIYKPLRPVYLTFTRRESSCEIKLWSTIPLEGIPA 267
          |         |         |         |         |         |         |         |         |         |
Db      126 QFEVVLODPRE--PRRATOMLKLNLIIPAPENMLTLKLSESOLELMWN---NRFLN 180
          |         |         |         |         |         |         |         |         |         |
Oy      268 RFEDYEIEIRED-DTLLVAIVE-NETTYLTKTNETROLCFVVRSKNYICSDGIJSEM 325
          |         |         |         |         |         |         |         |         |         |
Db      181 HOLEHLVQRTMDHSWTQSVDYRKHFSLPSVDGGKRTRFRKSRNPFLCGSNQHNMSEW 240
          |         |         |         |         |         |         |         |         |         |
Oy      326 SDKOCGEEDLSKTYLLRFWLPRGFILLIVIEVTG 360
          |         |         |         |         |         |         |         |         |         |
Db      241 SHPIHW-GSNTSKEN-----PFLFALEAVVISVG 268

RESULT 7
150455
Proactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
Accession: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
Session: 150455
[redacted]
Gen, X.; Horseman, N.D.
Endocrinology 135, 266-276, 1994
A>Title: Cloning, expression, and mutational analysis of the pigeon proactin receptor
A:Reference number: 150455; MUID:94283267; PMID:7516866
A:Accession: 150455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C:Superfamily: cytokine receptor homology <CRS1>
E:240-320/Domain: cytokine receptor homology <CRS1>
E:240-426/Domain: cytokine receptor homology <CRS2>
```

Query Match	10.3%	Score 216.5	DB 2	Length 830
Best Local Similarity	24.4%	Pred. No. 3.7e+09		
Matches 93	Conservative 53	Mismatches 174	Indels 61	Gaps 16

```

0Y 18 TTFGCTSSSDHIEKVNPNQDEHIDDPGLG-----LYLQW 53
    11 : : : : : : : : : : : : : : : : : : : : : :
Db 97 TTYNITVAMANEIGSNS-----DPQYVDVTSIVQDAPVNLSELTKTSATITYLLAKK 150
    11 : : : : : : : : : : : : : : : : : : : : : :
0Y 54 QPPLSLDHFKCIV-EYELKATNIGSETWKTITTKNLHYDGEDGLNKLEAKIHTLLPMO 112
    11 : : : : : : : : : : : : : : : : : : : : : :
Db 151 SPPLADVTSNHHYRYELRLPKEEKEMETV---SVGVOFYQYKVR-LOAQKYVVQYR 206
    11 : : : : : : : : : : : : : : : : : : : : : :
0Y 113 CTNSEVQSSNAETTYMISPG-IPEKVDQMDCVVYNNMQYLSCMKRPGIVGLVLDPTNYNL 171
    11 : : : : : : : : : : : : : : : : : : : : : :
F 207 CVLDIGSEWSESSERHHIHIPGSESPREKPTTIKCRSEKTEFTTCMKWPGSDGHPNITYTL 266
    11 : : : : : : : : : : : : : : : : : : : : : :
0Y 172 FYWYEGDLHAIQCVYIKADQNIQGFRRPLYEASDYKDFYICVNGSESENKPIRSSYFTFO 231
    11 : : : : : : : : : : : : : : : : : : : : : :
Db 267 LYSNEGEBRYVECDY-KTAGPN-SCYFDKKHHSFWITNYITKATNEIGSNSVSDPLYD 324
    11 : : : : : : : : : : : : : : : : : : : : : :
0Y 232 LQNIYKPLRPVYLLTFRESSCEIK---LKWS-IPLAGIPA-RCPDYELIREDPTTLY 284
    11 : : : : : : : : : : : : : : : : : : : : : :
Db 325 VTYIVQDFPVNVTLELKTNYRKRPLYLVLMSPPLADVBSGMLTLDYELRLMPEEA--- 381
    11 : : : : : : : : : : : : : : : : : : : : : :
0Y 285 TATVANEITYTLKTNETRQLCFVY---RSKVNIYCSDD--GIWSEKS-DKQCEWGEDIS 337
    11 : : : : : : : : : : : : : : : : : : : : : :
Db 382 -----EEMETIFVQOQTHYKMFSLNPGKATYVQIHCKRPDHHGSEWSELSKYUQIDPTDR 436
    11 : : : : : : : : : : : : : : : : : : : : : :
0Y 338 KKTLLRFLPGRGILLIVIV 358
    11 : : : : : : : : : : : : : : : : : : : : : :
Db 437 IKDNY-VWIVYGLSLSLCLV 456
    11 : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 8  
149280  
Interleukin-2 receptor gamma chain precursor - mouse  
C-Species: Mus musculus (house mouse)

C:Date: 27-Feb-1997 #sequence:revision 20-Jun-2000  
C:Accession: I49280; I49280; I49280; JN0775; I53388  
R:Caio, X.; Kozak, C.A.; Liu, Y.  
R:Caio, X.; Kozak, C.A.; Liu, Y.  
P:Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993  
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R)  
A:Reference number: A47514; MUID:93391374; PMID:8378320  
A:Accession: I49280

A: Molecule type: DNA  
A: Status: preliminary; translated from GB/EMBL/DBJ  
A: Residues: 1-369 <CAO>  
A: Cross-references: EMBL:U01795; NID:g727349; PIDN:AAA64279.1; PID:g727350  
Accession: M714

A:Accession: [AF17214](#)  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <RE2>  
 A:Cross-references: GB:L20048; NID:q404067; PIDD:AAA39286.1; PID:q404068

R; Kunaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K. *Biochem. Biophys. Res. Commun.* 193, 356-363, 1993

A: Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of fu

A: Reference number: JN0592; MUID: 93277575; PMID: 8503926

A:Accession: JN0592  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-369 <KQW>  
A:Cross-references: DDBJ:n13565, NID:nc0303684, PTDN:BA002760.1, PTD:nc0303685

A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.  
A:Reference number: IN0775; MUID:93366191; PMID:8359699  
R:Kodayashiki, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.  
Gene 130, 303-304, 1993

A:Accession: JN0775  
A:Molecule type: mRNA  
A:Residues: 1-369 <KOB>  
A:Cross-references: GB:DJ13821; NID:g436045; PIND:BAAO2974.1; PID:g436046  
B:Title: D. W. Deochand, et al. 2002

Richard, R.A.; Dougherty, G.J.  
submitted to the EMBL Data Library, October 1993  
A;Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain  
A;Reference number: S37582  
A;Accession: S37582

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>  
A:Cross-references: EMBL:X75337

Eur. J. Immunol. 24, 3014-3018, 1994  
 Article: The murine interleukin-2 receptor gamma chain gene: organization, chromosome  
 A:Reference number: 153398; MUID:95104285; PMID:7805729  
 Accession: 153398

A:Accession: J03370  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-369 <RES>  
 A:Cross-references: GB:S75852; NID:g861544; PIDN:AAB32904.1; PID:g86155

C:Genetics:  
A:Gene: IL-2Rgamma  
A:introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3  
C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHS2), bet

A: Description: receptor for interleukin-2  
 B: Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N  
 C: Superfamily: interleukin-2 receptor gamma chain  
 D: eptors.  
 E: Function:

C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein  
F.1-22/Domain: signal sequence #status predicted <SIG>  
F.23-366/Product: interleukin-2 receptor gamma chain #status predicted <MAT>  
F.256-284/Domain: transmembrane #status predicted <TM>

Query Match	10.1%	Score 212.5	DB 2	Length 369
Best Local Similarity	26.9%	Pred. No. 2.7e+09		

Matches	5' / 3'	conservative	43;	mismatches	116;	indels	23;	gaps	9;
Oy	136	PETKVQDVDDCYVNNQVLYLGSN---- <td>189</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	189						
Db	53	PTLPPEVQCVFNIEVNNCTWNSSEPOA-----TNTLLRYKRVASDNNNTFOCCSHLF	107						



A: Molecule type: mRNA  
A: Residues: 1-878 <ITO>  
R: Gorman, D.M.  
Submitted to GenBank, November 1989  
A: Reference number: A43022  
A: Accession: A43022  
A: Molecule type: mRNA  
A: Residues: 1-815, 'Q', 817-878 <GOR>  
A: Cross-references: GB:M29855; NID:g198342; PIDN:AAA3295.1; PID:g309406  
C: Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains receptors.  
C: Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology  
C: Keywords: cytokine receptor; duplication; transmembrane protein  
F: 1-72/Domain: signal sequence #status predicted <SIG>  
F: 23-878/Product: Interleukin-3 receptor beta chain #status predicted <MAT>  
F: 23-440/Domain: extracellular #status predicted <EXT>  
F: 39-236/Domain: cytokine receptor homology <CRS1>  
F: 254-433/Domain: cytokine receptor homology <CRS2>  
F: 441-462/Domain: transmembrane #status predicted <TM>  
F: 463-878/Domain: intracellular #status predicted <INT>

Query Match 9.3%, Score 195; DB 1; Length 878;  
Best Local Similarity 24.1%; Pred. No. 2e-07;  
Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

OY 34 PPDFEIVDPGYGLYLVIQWOPPL--SLDHFKETVEYELEKRNIGSEYTKITIKNLH 90  
||:| | | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 139 PPKDHIHPSPG-DHFLEWSVSLGDSQVSWLSKDIEFEVAAYKRL-QDSMED-AASLIH 193  
  
OY 91 YKDGDLKKGIKRIHTLLP-----WCCTNGSEVO-----SSMAETTYMISPGIPEY 138  
||:| | | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 194 -TSNQVN--LEPKL--FLPNSTIYAARVTRLSAASSLSGRPSRMSPEVHMDSOPG-DKA 247  
  
OY 139 KYVDNDCCYYVMQVLYLCESMKPGIGVLDTNYMLFYWEGELHALOCVVYIKADGONI--- 195  
||:| | | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 248 QPQNQCFCFDGQSILHCMEWMTQTGSVSFQLFRPSPAPEEKSGVVAHEPQASYTR 307  
  
OY 196 -GCRRPYLEASDYKDFYICVGNSSSENKPISRSYTFQLONIYKPLRPVY-LTFTRESSCE 253  
||:| | | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 308 YRCSLPVEPSPASHSQYTYSVKHLEGKEFI-MSYHIOME-----PPILOTKNRDS--- 357  
  
OY 254 IKLKMSIFLGIPACFP-VYEIEREDDTLTVTAVEN----EYTLKTINERPOLCFV 307  
||:| | | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 358 YSLHWETQKIP--KYIDHTFOVYKKRSSESKSRKDETEELGRVNSMDPQLPEPTSYCAR 414  
  
OY 308 VRSK-VNIYCSDDGJIMSEMSDKOCWEGEDLSKRTLEFWLPGFFLIIIVPTGILL 363  
||:| | | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 415 VRVKRISDY---DGIIMSERNXYTWI-TDWVWPTL---WI-----VLIIVFLLITLLL 460

RESULT 11  
A39255  
cytokine receptor common beta chain precursor - human  
C: Species: Homo sapiens (man)  
C: Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 02-Sep-1997  
C: Accession: A39255  
A: Reference number: A39255  
R: Proc. Natl. Acad. Sci. U.S.A., 87, 9655-9659, 1990  
A: Title: Molecular cloning of a second subunit of the receptor for human granulocyte A: Accession: A39255; MUID:91088571; PMID:1702217  
A: Molecule type: mRNA  
A: Residues: 1-897 <HAY>  
A: Cross-references: GB:M38275  
C: Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific C: Genetics:  
A: Gene: GDB:CSF2RB  
A: Cross-references: GDB:126838; OMTM:138981  
A: Map position: 22q13.1-22q13.1  
C: Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology  
C: Keywords: alternative splicing; cytokine receptor; duplication; transmembrane prote F: 1-16/Domain: signal sequence #status predicted <SIG>  
F: 17-897/Product: cytokine receptor commonbeta chain #status predicted <MAT>

F:17-443/Domain: extracellular #status predicted <EXT>  
 F:33-233/Domain: cytokine receptor homology <CRS1>  
 F:250-431/Domain: cytokine receptor homology <CRS2>  
 F:444-460/Domain: transmembrane #status predicted <TM>  
 F:461-697/Domain: intracellular #status predicted <INT>

Query Match 8.6%; Score 180.5; DB 1; Length 897;  
 Best Local Similarity 22.6%; Pred. No. 2.9e-06;

Matches 90; Conservative 58; Mismatches 146; Indels 105; Gaps 21;

32 VNPDPDEFIVPGYLG-----LYLQMP-----LSLDP----- 62

97 VIFQSEVYVDYDFSPDPPLGLTLVTLQHVQPEPPDLQISTDQHFLLTWVAL 156

63 -----KECTVEELKYRNGSETWK--TIITKNLHYKDGFLNKGIE-----A 103

157 GSPQSHMLSPEDLEFEVYKRL-QDSMEDAILLSNTS-----QATLGEPLHMSRTYVA 210

104 KIHT-LLPQCTNGSEVQSSMAETTYWISPOGIPETKYQDMCVYVMQYLLCSMKKEIG 162

211 RVRTPLAPGSLRSGR--PSKWSPEVCWDSQPG-DEAQPQNECFEDGAAVLSCSWEVAK 267

163 VLLDTNLFYWYEGDLHALQCVDIKADGONIG-----CRFPYLEASDYKDFYICVN 215

268 VASSVSSELFKPSPPDAGEECSPVLR---EGLSLHTRHHCQIPVDPATHGOIYVSQ 324

216 GSSBNKPIRSSYFTFQLONIYKPLPPVYLFTTRSSCEIKLWSIPLGPIPARCFDYIE 275

325 PRAEKHKHSV-----NI--QMAPSLANTKGD--SYSLRWEMMKRYEHIHDFEIQ 375

276 IREDDTLVATV-VENEYTYLTKTN-----ETROLCEV-VRSKVNITCSDDGIWSE 324

376 YRKD-----TATMKDSKTETLQNAHSMALPALPSTRYMAVRVTSRTGY---NGIWSE 427

325 WSDKQCEGDELSSKTLRFWLPFGFILLIYFTGLL 363

428 WSEARSMDESV-----LPMWVALIVITLTVAVL 457

# RESULT 12

Interleukin-3 receptor beta-subunit - rat

C/Species: Rattus sp. (rat)

C/Date: 26-Jul-1996 #sequence, revision 26-Jul-1996 #text, change 23-Jul-1999

C/Accession: I56563

R/Appel, K.; Buttin, M.; Sauter, A.; Gebicke-Haerter, P. J.

J. Neurosci. 15, 5800-5809, 1995

A>Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and

A/Reference number: I56563; MUID:95370942; PMID:7643220

A/Accession: I56563

A>Status: preliminary; translated from GB/EMBL/DDAJ

A/Molecule type: mRNA

A/Residues: 1-896 <RES>

A/Cross-references: GB:579263; NID:g1086954; PIDN:AA835068.1; PID:g1086955

C/Genetics:

A/Gene: IL-3beta

C/Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology

C/Keywords: cytokine receptor

F:33-235/Domain: cytokine receptor homology <CRS1>

F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 8.5%; Score 178; DB 2; Length 896;

Best Local Similarity 21.4%; Pred. No. 4.6e-06;

Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

5 CLAIGCL-VT-FLISTFGCTSSDTEIKV-----PPQDFELVDPGYLGL 49

94 CVPRRCVLPYQSVSSEDYSLQPDRLSLVLAQHVQPPPKDISISPG--DHF 151

50 YLQMPPLV--SLDHFECTVEELKYRNGSETWKTITITKNLHYKDGFLNKGIEAKIH 106

152 LTKASVPLGDAQVSLLSOKDLQFEVAVKQL-QDSMED--ASSLH-----TCNLMTLEPK 203

QY 107 TLIP-----NQTNGSEVQ--SSMAETTYWISPOGIPETKYQDMCVYVMQYLL 154

204 LELNRSIYAVRROLAPGSSLSGRPSGMSPEVHSDPTE--DKARPOLQCFQGIOSL 262

155 CSMPKPGICVLDITVYNLFYWYEGDLHALQCVDIKADGONIGCRFPYLEASDYKDFYICV 214

263 CSWEWTKVTVDSVSFGLEYS SSPKAGEKCCSPVKE-----LQASRYTRYICSL 311

QY 215 NGSENKPIRSSYFTFQLO-----NIKVPPLP-VYLTFTRESSCEIKLWSIPL 262

312 NVSD--PAHSQYTVSVKRLDQKGFIESFNHQMNPPLTLTKNRDS---YSLHMETQK 365

263 GPAPARCFDYIEIR-----EDDTLVATVAVENETYLTKTNETROLCEVRSKVNITC 316

366 MSYPIQAHFQVQYKKKLDREWSKT-----ENLHAHSMDLPOLEPGSYCARVAVTIP 421

QY 317 SDDIWSRSDKQCEGDELSSKTLRFWLPFGFILLIYFTGLL 363

422 EYKGLWSEMSNECWT-TDWVMPPL--WI--VLIIVFLIPL 460

# RESULT 13

Cytokine receptor common beta chain precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1993 #sequence, revision 30-Jun-1993 #text, change 22-Jun-1999

C/Accession: A35782

R/Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Araki,

A>Title: Cloning and expression of a gene encoding an interleukin 3 receptor-1-like pro

A/Reference number: A35782; MUID:90319131; PMID:1695379

A/Accession: A35782

A/Molecule type: mRNA

A/Residues: 1-896 <GOR>

A/Cross-references: GB:M34397; NID:g191821; PIDN:AA37204.1; PID:g309101

C/Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 rece

C/Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology

C/Keywords: cytokine receptor; duplication; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>

F:23-441/Domain: extracellular #status predicted <EXT>

F:33-235/Domain: cytokine receptor homology <CRS1>

F:253-434/Domain: cytokine receptor homology <CRS2>

F:442-463/Domain: transmembrane #status predicted <TM>

F:464-996/Domain: intracellular #status predicted <INT>

Query Match 8.2%; Score 173.5; DB 1; Length 896;

Best Local Similarity 20.7%; Pred. No. 1e-05;

Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

5 CLAIGCLVTEFLISTFGCTS-----SSDTEIK-----VNPDPDEFIVDPGYLG 48

94 CVPRRCVLPY---TRFTSTNEDYSFRPDSDLQGLWVPLAQNQVPLPKVSSSEDR 150

49 LYLQMPPLV--SLDHFECTVEELKYRNGSETWKTITITKN-----LHYKDGFLNKG 100

151 FILEMSVSLGDAQVSWLSKDIIEFEVAVKRL-QDSMEDAVSLHRSKROVNEPFLFPPNS 209

QY 101 IEA-KIHT-LLPQCTNGSEVQSSMAETTYWISPOGIPETKYQDMCVYVMQYLLCSMK 158

210 IYAPRVTRLPYSGSSLSGR--PSKWSPEAHWDSPG-DKADPOLQCFQGIOSLCSWE 266

159 PGICVLLDTNYNLFYWYEGDLHALQCVDIK-ADGONI-----GCRFPYLEASDYKDFYIC 213

267 VMPTGTSVSRGLFRRSPVAPAEKSPVYKEPGASVYVYRHCSLVPPEPSAHQYTVS 326

QY 214 VNGSENKPIRSSYFTFQLONIYKPLPPVYLFTTRSSCEIKLWSIPLGPIPARCFDYIE 273

327 V-----KHLQGGKFIIMSYNHQMEPPLINTLNKRD--SYSLHWEQKMAVSFEIHTFQ 377

QY 274 IEIREDDTLVATVAVEN--ETTYLTKTNETROLCEVRSKVNITCSDDGIMSEMSDQCV 331

378 VOYKKKSDSWEDSKTEMLDRAHSMDSLSQLEPDTISYCARVAVKPKISNYDGIWMSKEEYTW 437

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OY      332  EGEDLSKTTLLRFWLPFGFILLIVFTGILL 363
          :  |  |  |  |  |  |  |  |  |  |  |
Db      438  K-TDWVMPFL--WI----VLLIVFLITLL 461

```

RESULT 14  
A29884

prolactin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 28-Jul-2000  
C:Accession: A29884  
R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Egerly, M.; Shiota, M.; Banville  
Cell 53, 69-77, 1988  
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho  
A:Reference number: A29884; MUID:88165059; PMID:2832068  
A:Accession: A29884  
Molecule type: mRNA  
Residues: 1-310 <BOU>  
C:Cross-references: GB:M19304; NID:g206364; PIDN:AAAA1937.1; PID:g206365  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-310/Product: prolactin receptor #status predicted <MAT>  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match	7.8%;	Score 165;	DB 2;	Length 310;
Best Local Similarity	28.5%;	Pred. No. 1.3e-05;		
Matches 63;	Conservative 24;	Mismatches 94;	Indels 40;	Gaps 10;

QY 131 SPQGIPETKVDDMCYVYNNQYLICSKKPGIGVLLDTNNLFIWYEGDLHALQCVDIYKA 190

DB 21 SPQGRPEIH----KCSPPDKERFTTCWNNPBGTDGGLPTNYSLTYSKGEKTTYECSPDY-KT 75

191 DGQNGICRFPYLEASDYKDFYICVN-----GSSENKPIRSSSYTFPOLQNIWKPLEPVYLT 245

QY 246 F-----TRESSCETIKLWSIP-LGPIPARCFDEIETREDTTLVATAVENETYILKTNE 300C  
::: :||| : :|||

DD 130 DEVRQENDANKILMWNMSFPIIDVNVIGWFIMEIEIK-----L  
QY 301 TROL-----CFVVRSKVNIYCSDDGITWSEMSDKOCWE 332

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183 QTFKVFDLYPGQKYLVQTRCK--PDHGYSRWSQESSVE 2200

```

RESULT 15

prolactin receptor Nb2 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)

C;Accession: A41070; I55417  
R;All, S.; Pellegrini, I.; Kelly, P.A.  
I. Biol. Chem. 266: 20110-20117, 1991

A:Title: A prolactin-dependent immune cellline (Nb2) expresses a mutant form of prolactin receptor  
A:Reference number: A41070; MUID:92041834; PMID:1718958  
A:Accession: A41070

A:Residues: 1-412 <ALI>  
A:Molecule type: mRNA  
A:Cross-references: GB:M74152: PTD:AAA41946.1: PTD:Q206390  
NID:Q206389:

J. Biol. Chem. 269, 26076-26082, 1994

A;Accession: I55417  
A;Status: translated from GB/EMBL/DBJ  
nucleotide number: 155411, hold: 5501432, fmid: 1525513

A:Residues: 1-412 <RES>  
A:Cross-references: EMBL:U07567; NID:9641963; PIDN:AAA61784.1; PID:9641964

C;Superfamily: cytokine receptor homology  
C;Keywords: transmembrane protein

F;31-216/Domain: cytokine receptor homology &lt;CRS&gt;

Query Match	7.8%;	Score 165;	DB 2;	Length 412;
Post Local Similarity	30.5%	Score 1000;	DB 1;	Length 1000;

Matches	63;	Conservative	24;	Mismatches	94;	Indels	40;	Gaps	10;
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QY 131 SPGIPETKVDMDCVYYNMQYLLCSMKRGIGVLLDTNINLFYWEGLDHALOCVDYIKA 190

191 DGONIGCRPYLEASDYKDEYICVN-----GSSENKPIRSSYFTFOLQNIKPLPPVYL 245

00  
Db /6 SCGN-SCFFSKQYTSIMKRIIITVNATNQMGSSSSDPL-----YVDVTVIIEBPBRNLT 129  
246 F-----TRSSCETIKLKWSTP-I GPIPARCEDYEIETREDTTIIVATVENETVATIKTNE 3000

Db 130 LEVQQLDKDKTYLWVKWSPTITDVKTGNTMEYEIR-----LKPEAEENEIHTFGH 182

Db 183 QTFKVEDLIPGQKYLVTQTRCK--PDHGYSRWSQESSVE 2200

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Job time : 24 secs

Job time : 24 secs

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search completed:  Sunday 24 / 2009, 15:37:32
Job time : 24 secs

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